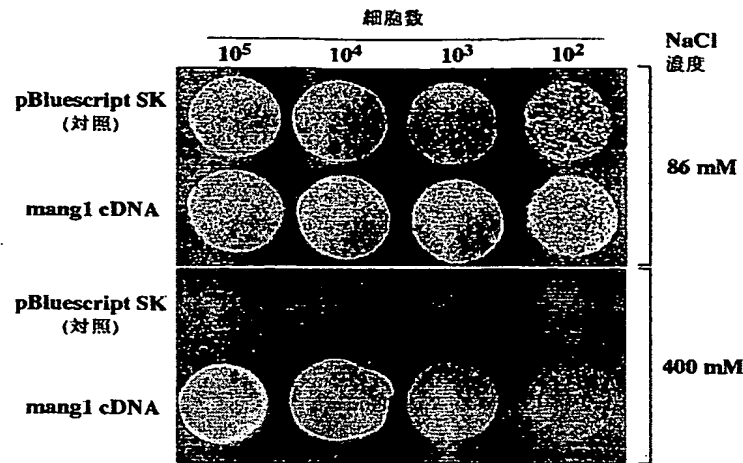
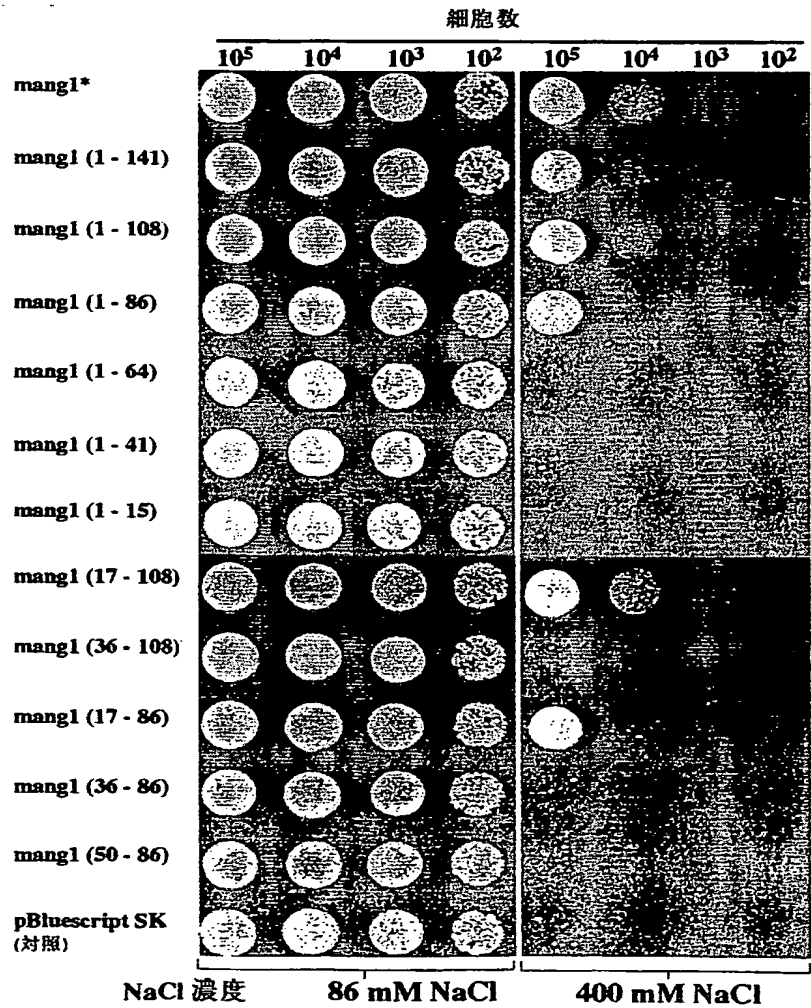


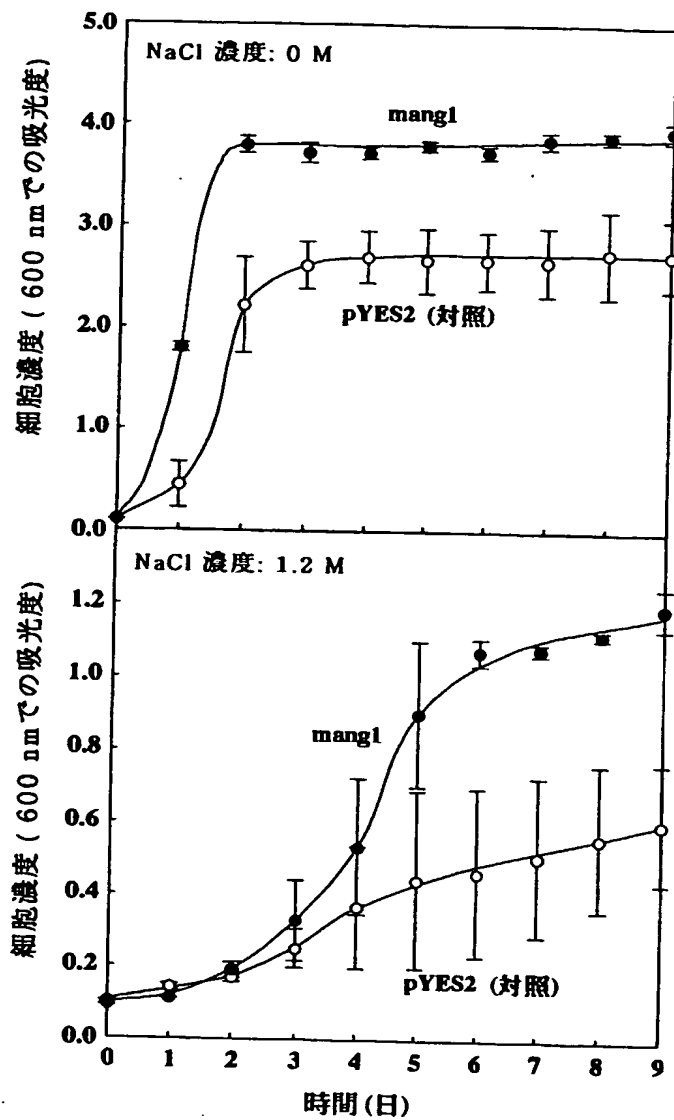
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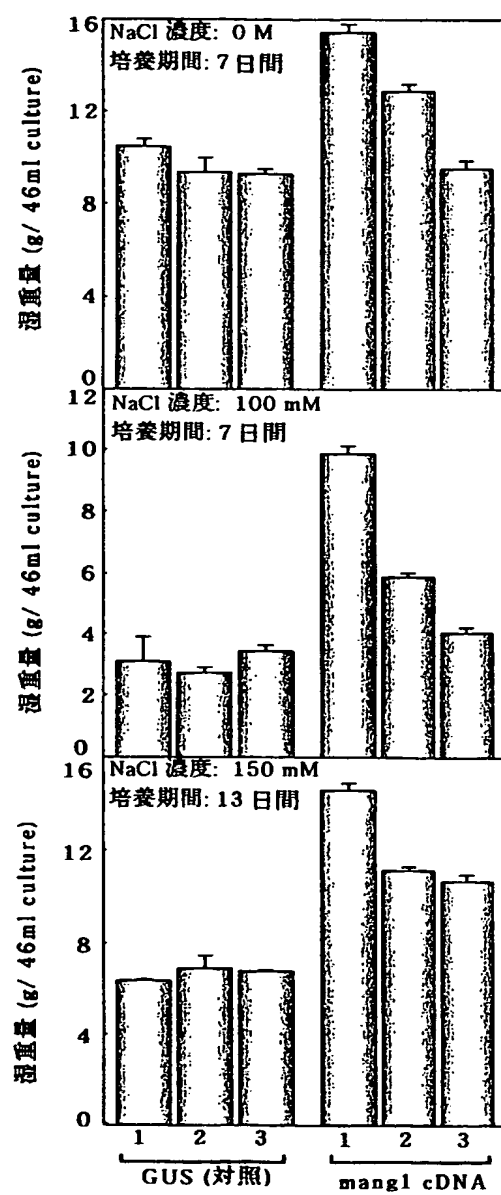
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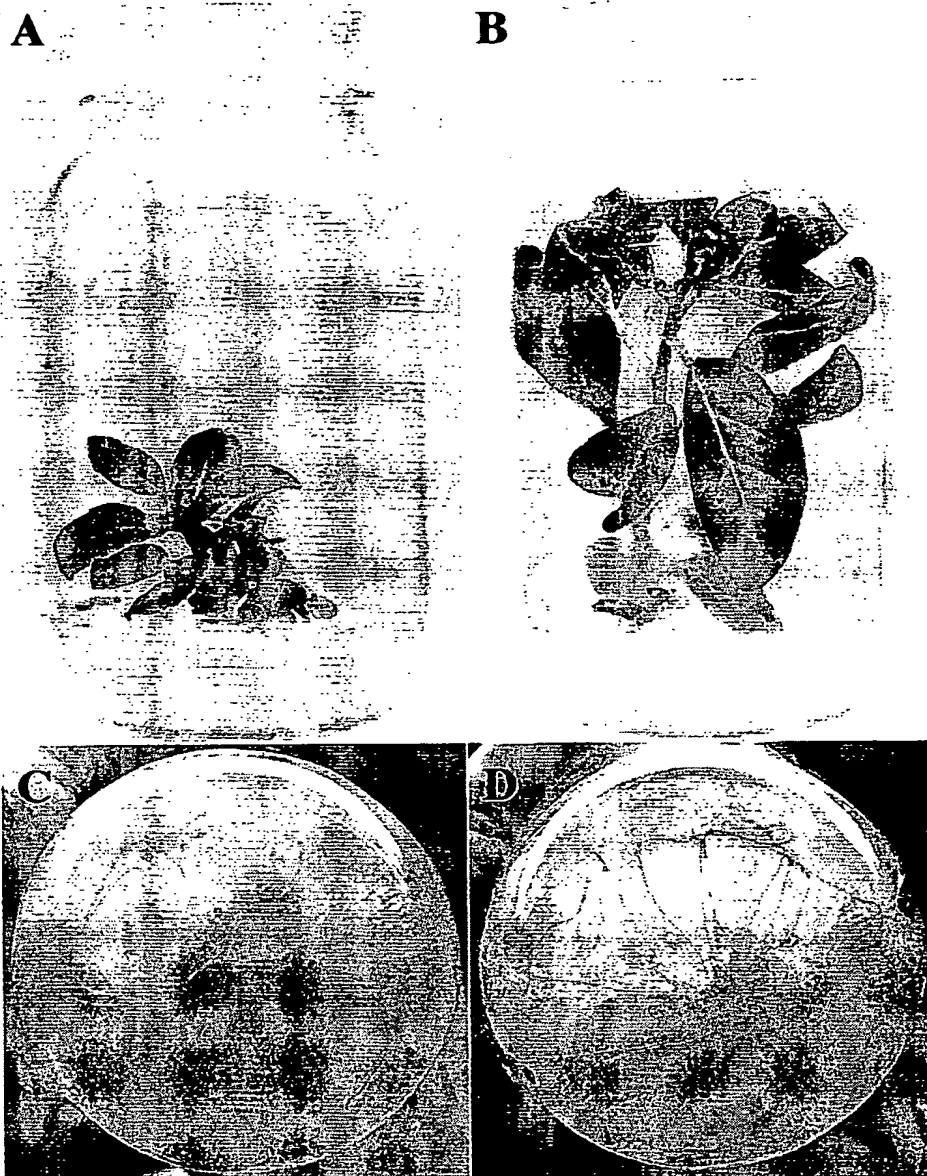
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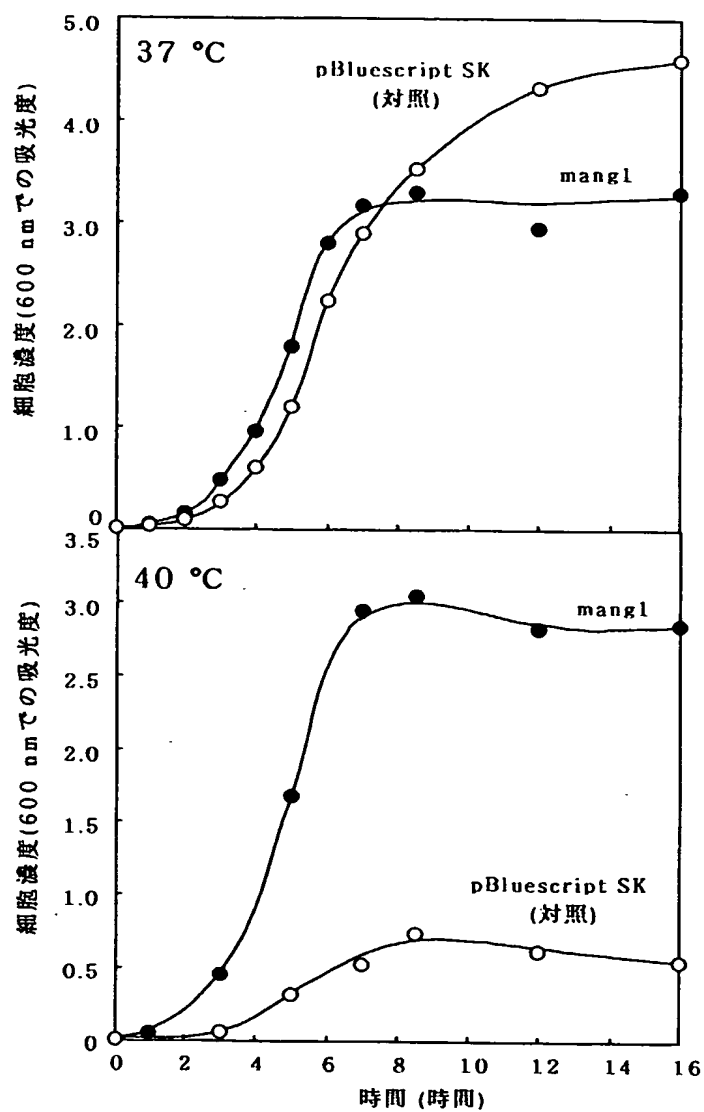
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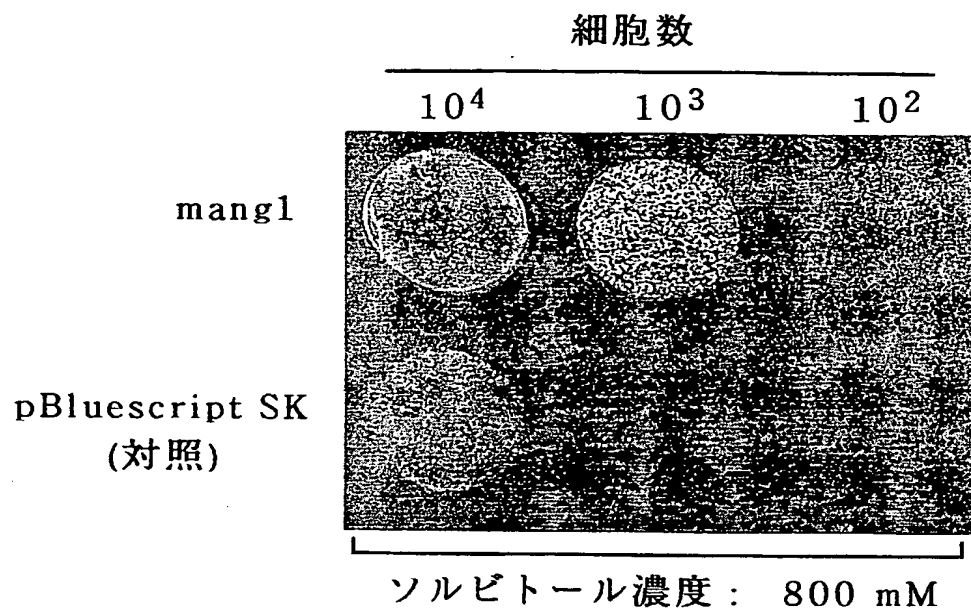
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第 6 図

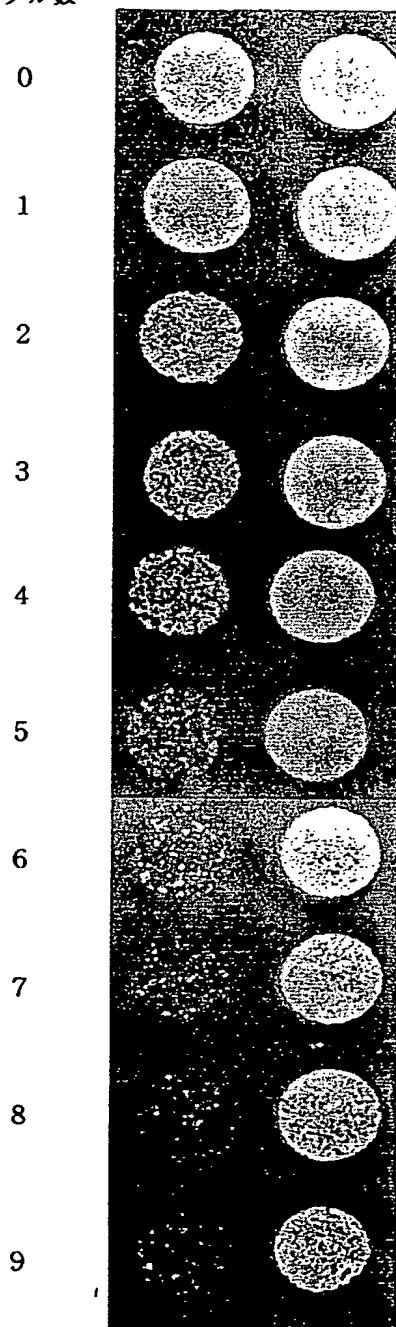


## 第 7 図



## 第 8 図

凍結/融解 pBluescript SK mangl  
サイクル数 (対照)



## 第 9 図

## 塩基配列の比較

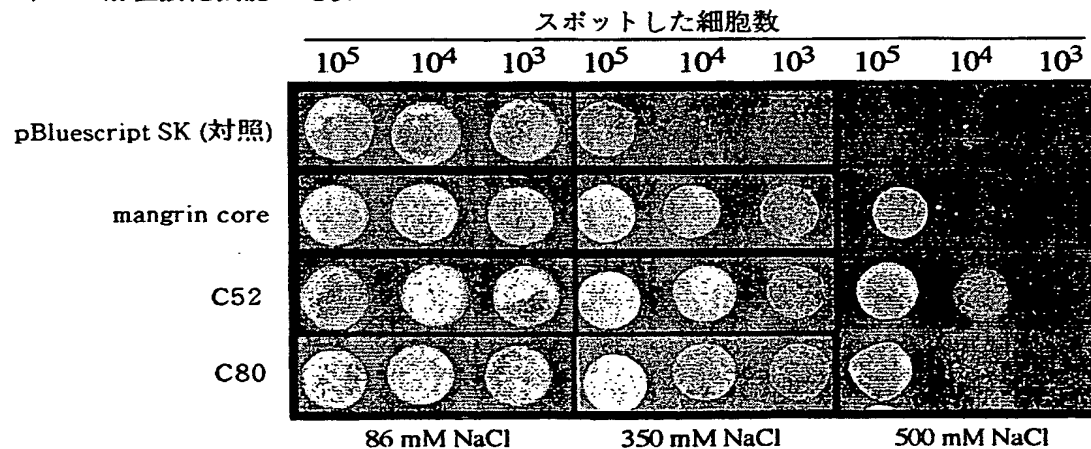
mangrin core	1	ATGAAGGTGGTCGGCCCTGCAAGATCAAAGAGTGCTACTGTACCCACCCAAACAGTATTG	60
C-52	1	ATGAAGGTGGTCGGCCCTGCAAGATCAAAGAGTGCTACTGTACCCACCCAAACAGTATTG	60
C-80	1	ATGAAGGTGGTCGGCCCTGCAAGATCAAAGAGTGCTACTGTACCCACCCAAACAGTATTG	60
mangrin core	61	CCTTTCAAGTTTCAAAACCCGTCGTTACTCACTCGATCGCTAAGCTTTTCATCAAAAGGT	120
C-52	61	CCTTTCAAGTTTCAAAACCCGTCGTTACTCACTCGATCGCTAAGCTTTTCATCAAAAGGT	120
C-80	61	CCTTTCAAGTTTCAAAACCCGTCGTTACTCACTCGATCGCTAAGCTTTTCATCAAAAGGT	120
mangrin core	121	TCAAGCTTTGACAGCTTCTCTGTACCCAAAAGATCTTTTTCTTGAGAAGCCAAGCCACT	180
C-52	121	TCAAGCTTTGACAGCTTCTCTGTACCCAAAAGATCTTTTTCTTGAGAAGCCAAGCCACT	180
C-80	121	TCAAGCTTTGACAGCTTCTCTGTACCCAAAAGATCTTTTTCTTGAGAAGCCAAGCCACT	180
mangrin core	181	CCATCTGATGATGCCTCAAGACCCACCAAAGTTCAAGAGCTGTAA	225
C-52	181	CCATCTGATGATGCCTCAAGACCCACCAAAGTTCAAGAGCTGTAA	225
C-80	181	CCATCTGATGATGCCTCAAGACCCACCAAAGTTCAAGAGCTGTAA	225

## アミノ酸配列の比較

mangrin core	1	MKVVGPARSKSATVPTQTVLPFKFTNPSSLTRSLSFSSKGSFDSFSVPKRFSFSCRQAT	60
C-52	1	MKVVGPARSKSATVPTQTVLPFKFTNPSSLTRSLSFSSKGSFDSFSVPKRFSFSCRQAT	60
C-80	1	MKVVGPARSKSATVPTQTVLPFKFTNPSSLTRSLSFSSKGSFDSFSVPKRFSFSCRQAT	60
mangrin core	61	PSDDASRPTKVQEL	74
C-52	61	PSDDASRPTKVQEL	74
C-80	61	PSDDASRPTKVQEL	74

## 第 10 図

## 塩ストレス耐性強化機能の比較





## SEQUENCE LISTING

<110> JAPAN SCIENCE AND TECHNOLOGY CORPORATION

<120> Screening of genes to give tolerance against  
environmental stress and the applications

<130> 12-130

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<150> JP P1999-235910

<151> 1999-07-19

<150> JP P2000-85377

<151> 2000-03-24

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Arg Ser Lys Ser Ala Thr Val Pro Thr Gln Thr Val Leu Pro Phe Lys
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Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser Arg Pro Thr Lys Val			
70	75	80	85
caa gag ctg tgt gtg tat gag atg aac gag aga gat cgt gga agc cct			344
Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg Asp Arg Gly Ser Pro			
90	95	100	
gct gtt ctg cgg ttg agc cag aaa cct gtt aat tct ctg ggc gat ctg			392
Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn Ser Leu Gly Asp Leu			
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gtg cct ttc agt aac aaa gtt tac agc gga gac ctg cag aag cga att			440
Val Pro Phe Ser Asn Lys Val Tyr Ser Gly Asp Leu Gln Lys Arg Ile			
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Gly Val Thr Ala Glu Tyr Ala Ser			
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 35 40 45

Ser Phe Ser Ser Lys Gly Ser Ser Phe Asp Ser Phe Ser Val Pro Lys  
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Arg Ser Phe Ser Cys Arg Ser Gln Ala Thr Pro Ser Asp Asp Ala Ser  
 65 70 75 80

Arg Pro Thr Lys Val Gln Glu Leu Cys Val Tyr Glu Met Asn Glu Arg  
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Asp Arg Gly Ser Pro Ala Val Leu Arg Leu Ser Gln Lys Pro Val Asn  
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Gly Glu Arg Gln Ser Gly Gln Asp Val Arg Thr Gln Asn Val Val Ala
15 20 25

lgt caa gcg gtt gcc aat att gtc aaa tct tca ctt ggt cct gtc gga 209
Cys Gln Ala Val Ala Asn Ile Val Lys Ser Ser Leu Gly Pro Val Gly
30 35 40

ctc gac aag atg cta glg gat gat att ggt gat gta aca att aca aat 257
Leu Asp Lys Met Leu Val Asp Asp Ile Gly Asp Val Thr Ile Thr Asn
45 50 55

gat ggt gct acg att ctt aag atg tta gaa gla gag cat cct gca gca 305
Asp Gly Ala Thr Ile Leu Lys Met Leu Glu Val Glu His Pro Ala Ala
60 65 70 75

aag glg ctc gtg gag ttg gct gag ctt caa gac cga gaa gtt gga gat 353
Lys Val Leu Val Glu Leu Ala Glu Leu Gln Asp Arg Glu Val Gly Asp
80 85 90

gga acc act tcg gtt gtc atc ata gca gct gag ttg ctc aag aga gca 401
Gly Thr Thr Ser Val Val Ile Ile Ala Ala Glu Leu Leu Lys Arg Ala
95 100 105

aat gat ctc gtg agg aat aag atc cac cca aca tca ata atc agt gga 449
Asn Asp Leu Val Arg Asn Lys Ile His Pro Thr Ser Ile Ile Ser Gly
110 115 120

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Tyr Arg Leu Ala Met Arg Glu Ala Cys Lys Tyr Val Glu Glu Lys Leu
125 130 135

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140 145 150 155

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Lys Thr Ser Met Ser Ser Lys Leu Ile Ala Gly Asp Ser Asp Phe Phe
160 165 170

gca aat ttg gtt gla gat gct gla caa gca gla aag atg acc aat gca 641
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His Gly Lys Ser Ala Arg Asp Ser Cys Leu Leu Asn Gly Tyr Ala Leu			
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Asn Thr Gly Arg Ala Ala Gln Gly Met Pro Met Arg Val Ala Pro Ala			
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agg att gct tgt ctt gac ttt aat ctt cag aaa acg aag atg caa ttg			833
Arg Ile Ala Cys Leu Asp Phe Asn Leu Gln Lys Thr Lys Met Gln Leu			
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Gln Arg Glu Ala Asp Met Thr Lys Glu Arg Ile Glu Lys Leu Leu Lys			
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Ala Gly Ala Asn Val Val Leu Thr Thr Lys Gly Ile Asp Asp Met Ala			
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ctt aaa tai ttt gtg gag gct ggg gct att gct gtg aga cgt gtt cgg			1025
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aaa gag gat atg cgc cat gtt gcc aag gca act ggt gca aca ctg gtt			1073
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Phe Ala Glu Ser Leu Leu Ile Ile Pro Lys Val Leu Ala Val Asn Ala	
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Ala Lys Asp Ala Thr Glu Leu Ala Ala Lys Leu Arg Ala Tyr His His	
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Thr Ala Gln Thr Lys Ala Asp Lys Lys His Leu Ser Ser Met Gly Leu	
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Glu Pro Ala Met Ser Lys Ile Lys Ile Ile Gln Phe Ala Thr Glu Ala	
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Ala Ile Thr Ile Leu Arg Ile Asp Asp Met Ile Lys Leu Val Lys Asp	
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Val Leu Thr Thr Lys Gly Ile Asp Asp Met Ala Leu Lys Tyr Phe Val		
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His Val Ala Lys Ala Thr Gly Ala Thr Leu Val Ser Thr Phe Ala Asp		
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Glu Val Val Glu Glu Arg Ile Ala Asp Asp Asp Val Ile Met Ile Lys		
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Gly Thr Lys Thr Thr Ser Ala Val Ser Leu Ile Leu Arg Gly Ala Asn		
	370 375	380



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 485 490 495  
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Ile Gly Ala Glu Thr Ser Leu Arg Tyr Ala Ile His Leu Ile Thr Ala	
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 gagccctgaa atgaagaaca atggtagact tggatcccac ctggccctt atgatatct 1122  
 tctggaatlg aaaaaagagt ccaagaaatt tgaatttcat gaaattggag aactgaactg 1182  
 tgcttactaa attgctactt tgcaagtaat gatagggcac tcacgcttga ctggctaagt 1242  
 atttatgttt ttaicalcaa aaaaaaaaaa aaaaaaaaaa 1280

&lt;210&gt; 8

&lt;211&gt; 334

&lt;212&gt; PRT

&lt;213&gt; Bruguiera sexangula

&lt;400&gt; 8

Ile Glu Gly Glu Val Val Glu Val Gln Ile Asp Arg Pro Ala Val Thr  
 1                      5                      10                      15

Gly Ala Ala Ser Lys Thr Gly Lys Leu Thr Leu Lys Thr Thr Glu Met  
 20                      25                      30

Glu Thr Val Tyr Asp Leu Gly Ala Lys Met Ile Glu Ala Leu Gly Lys  
 35                      40                      45

Glu Lys Val Gln Ser Gly Asp Val Ile Ala Ile Asp Lys Ala Ser Gly  
 50                      55                      60

Lys Ile Thr Lys Leu Gly Arg Ser Phe Ser Arg Ser Arg Asp Tyr Asp  
 65                      70                      75                      80

Ala Met Gly Pro Gln Val Lys Phe Val Gln Cys Pro Asp Gly Glu Leu  
85 90 95

Gln Lys Arg Lys Glu Val Val His Cys Val Ser Leu His Glu Ile Asp  
100 105 110

Val Ile Asn Ser Arg Thr Gln Gly Phe Leu Ala Leu Phe Thr Gly Asp  
115 120 125

Thr Gly Glu Ile Arg Ala Glu Val Arg Glu Gln Ile Asp Thr Lys Val  
130 135 140

Ala Glu Trp Arg Glu Glu Gly Lys Ala Glu Ile Val Pro Gly Val Leu  
145 150 155 160

Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser Phe Leu  
165 170 175

Asn Arg Ala Leu Glu Asn Glu Met Ala Pro Ile Leu Val Val Ala Thr  
180 185 190

Asn Arg Gly Ile Thr Thr Ile Arg Gly Thr Asn Tyr Lys Ser Pro His  
195 200 205

Gly Ile Pro Ile Asp Leu Leu Asp Arg Leu Leu Ile Ile Thr Thr Gln  
210 215 220

Pro Tyr Thr Lys Asp Glu Ile Arg Lys Ile Leu Asp Ile Arg Cys Gln  
225 230 235 240

Glu Glu Asp Val Glu Met Ala Glu Glu Ala Lys Ala Leu Leu Thr His  
245 250 255

Ile Gly Ala Glu Thr Ser Leu Arg Tyr Ala Ile His Leu Ile Thr Ala  
260 265 270

Ala Ala Leu Ala Cys Gln Lys Arg Lys Gly Lys Leu Val Glu Thr Glu  
275 280 285

Asp Ile Ser Arg Ala Tyr Asn Leu Phe Leu Asp Val Lys Arg Ser Thr  
290 295 300

Gln Tyr Leu Ile Glu Tyr Gln Asn Gln Tyr Met Phe Asn Glu Ala Pro  
305 310 315 320

Val Gly Glu Gly Asp Glu Glu Gly Ala Asn Ala Met Leu Ser

325

330

<210> 9  
 <211> 420  
 <212> DNA  
 <213> *Bruguiera sexangula*

<220>  
 <221> CDS  
 <222> (27)..(194)

<400> 9  
 cgaaagtata aagtatcg cgagcg atg ggt cac tct aac gtc tgg aac tct 53  
 Met Gly His Ser Asn Val Trp Asn Ser  
 1 5

cac ccc aag aac tac ggc cct ggt tcc cgc gcc tgt cgg gtg tgt ggg 101  
 His Pro Lys Asn Tyr Gly Pro Gly Ser Arg Ala Cys Arg Val Cys Gly  
 10 15 20 25

aat ccg cac ggg ttg atc agg aag tac gga ctc atg tgc tgc aga cag 149  
 Asn Pro His Gly Leu Ile Arg Lys Tyr Gly Leu Met Cys Cys Arg Gln  
 30 35 40

tgc ttc cgt agc aat gcc aag gaa att ggc ttc att aag tac cgc 194  
 Cys Phe Arg Ser Asn Ala Lys Glu Ile Gly Phe Ile Lys Tyr Arg  
 45 50 55

tgaatgatat cgaatggcc cagaatggcc tgtggcgggtg cgtgttcgat ttcagtagtt 254

cccccttttc ggaatgagcct taggacaatg ttctcttttag tttatgtatt gtgaacttg 314

gacgatgttt gaactaacga tatcttgga tcatltigata tttcgagagt ttattatltt 374

gatcatcatc ctcttgcctc tctgcctaaa aaaaaaaaaa aaaaaa 420

<210> 10  
 <211> 56  
 <212> PRT  
 <213> *Bruguiera sexangula*

<400> 10  
 Met Gly His Ser Asn Val Trp Asn Ser His Pro Lys Asn Tyr Gly Pro

1	5	10	15
Gly Ser Arg Ala Cys Arg Val Cys Gly Asn Pro His Gly Leu Ile Arg			
	20	25	30
Lys Tyr Gly Leu Met Cys Cys Arg Gln Cys Phe Arg Ser Asn Ala Lys			
	35	40	45
Glu Ile Gly Phe Ile Lys Tyr Arg			
	50	55	

<210> 11  
 <211> 1664  
 <212> DNA  
 <213> *Bruguiera sexangula*

<220>  
 <221> CDS  
 <222> (34).. (1380)

<400> 11  
 tcctctctttaa cagggttaaag ctaagacitit ata atg ggt aag gag aag att cac 54  
 Met Gly Lys Glu Lys Ile His  
 1 5

att aac att gtg gtt att ggc cat gtc gac tcc gga aag tca acc aca 102  
 Ile Asn Ile Val Val Ile Gly His Val Asp Ser Gly Lys Ser Thr Thr  
 10 15 20

act ggc cac ttg att tac aag ctt gga ggt atc gac aag cgt gtg att 150  
 Thr Gly His Leu Ile Tyr Lys Leu Gly Gly Ile Asp Lys Arg Val Ile  
 25 30 35

gag agg ttt gag aag gaa gct gct gag atg aac aag agg tca ttc aag 198  
 Glu Arg Phe Glu Lys Glu Ala Ala Glu Met Asn Lys Arg Ser Phe Lys  
 40 45 50 55

tat gcc tgg gtg ctt gac aag ctg aag gct gag cgt gag cgt ggt atc 246  
 Tyr Ala Trp Val Leu Asp Lys Leu Lys Ala Glu Arg Glu Arg Gly Ile  
 60 65 70

acc att gat att gcc ttg tgg aag ttc gag aca acc aaa tat tac tgc 294  
 Thr Ile Asp Ile Ala Leu Trp Lys Phe Glu Thr Thr Lys Tyr Tyr Cys  
 75 80 85



acg gtc att gal gct cct gga cat cgt gac ttt att aag aat atg atc 342  
 Thr Val Ile Asp Ala Pro Gly His Arg Asp Phe Ile Lys Asn Met Ile  
 90 95 100

acc ggg act tcc caa gct gac tgt gct glc ctc atc att gac tct acc 390  
 Thr Gly Thr Ser Gln Ala Asp Cys Ala Val Leu Ile Ile Asp Ser Thr  
 105 110 115

act ggt ggc ttt gag gct ggt atc tct aaa gat ggt cag acc cgc gag 438  
 Thr Gly Gly Phe Glu Ala Gly Ile Ser Lys Asp Gly Gln Thr Arg Glu  
 120 125 130 135

cat gcc ctg ctt gcc ttc acc ctt ggt gtt aag caa atg att tgc tgc 486  
 His Ala Leu Leu Ala Phe Thr Leu Gly Val Lys Gln Met Ile Cys Cys  
 140 145 150

tgc aac aag atg gat gct acc act tcc aag tat tct aag gca aga tat 534  
 Cys Asn Lys Met Asp Ala Thr Thr Ser Lys Tyr Ser Lys Ala Arg Tyr  
 155 160 165

gat gaa att gtt aag gaa gtg tca tcc tac ttg aag aag gtt ggt tac 582  
 Asp Glu Ile Val Lys Glu Val Ser Ser Tyr Leu Lys Lys Val Gly Tyr  
 170 175 180

aac cca gag aag att cct ttt gtc ccc ata tct gga ttt gag ggt gac 630  
 Asn Pro Glu Lys Ile Pro Phe Val Pro Ile Ser Gly Phe Glu Gly Asp  
 185 190 195

aac atg att gag aga tcc acc aac ctt gac tgg tac aag ggc cca act 678  
 Asn Met Ile Glu Arg Ser Thr Asn Leu Asp Trp Tyr Lys Gly Pro Thr  
 200 205 210 215

ctt ctt gag gcc ctg gac atg atc cag gag cca aag agg cca tca gat 726  
 Leu Leu Glu Ala Leu Asp Met Ile Gln Glu Pro Lys Arg Pro Ser Asp  
 220 225 230

aag ccc ctc cgt ctc cca ctt cag gat gtg tac aag att ggt ggt att 774  
 Lys Pro Leu Arg Leu Pro Leu Gln Asp Val Tyr Lys Ile Gly Gly Ile  
 235 240 245

ggg aca gtc cca gtg ggt cgt gtt gaa act ggt glc ctg aag cct gga 822  
 Gly Thr Val Pro Val Gly Arg Val Glu Thr Gly Val Leu Lys Pro Gly  
 250 255 260

atg gtt gtt act ttt ggt ccc tca gga ctg acc act gaa gtt aag tct 870

Met Val Val Thr Phe Gly Pro Ser Gly Leu Thr Thr Glu Val Lys Ser	
265 270 275	
gtg gag atg cac cat gaa gct ctc caa gag gct ctt ccc gga gac aac	918
Val Glu Met His His Glu Ala Leu Gln Glu Ala Leu Pro Gly Asp Asn	
280 285 290 295	
glt ggc ttc aat gtt aag aat gtt tcc glg aag gat ctt aag cgg ggt	966
Val Gly Phe Asn Val Lys Asn Val Ser Val Lys Asp Leu Lys Arg Gly	
300 305 310	
tat gtt gcc tca aac tcc aag gat gat cct gcc aag gag gca tct agc	1014
Tyr Val Ala Ser Asn Ser Lys Asp Asp Pro Ala Lys Glu Ala Ser Ser	
315 320 325	
ttc acc tcc caa gtt atc atc atg aac cac cct ggt cag att gga aat	1062
Phe Thr Ser Gln Val Ile Ile Met Asn His Pro Gly Gln Ile Gly Asn	
330 335 340	
ggt tat gcc cct gtt ctg gat tgc cac acc tct cac att gct gtc aag	1110
Gly Tyr Ala Pro Val Leu Asp Cys His Thr Ser His Ile Ala Val Lys	
345 350 355	
ttt tct gag atc ctc aca aag att gat agg cga tct ggc aag gag ctt	1158
Phe Ser Glu Ile Leu Thr Lys Ile Asp Arg Arg Ser Gly Lys Glu Leu	
360 365 370 375	
gaa aag gag ccc aag ttc ttg aag aat ggt gat gct ggg ttc glg aag	1206
Glu Lys Glu Pro Lys Phe Leu Lys Asn Gly Asp Ala Gly Phe Val Lys	
380 385 390	
atg att ccg acc aag cct atg gtg gtg gaa act ttc tcc gag tat cct	1254
Met Ile Pro Thr Lys Pro Met Val Val Glu Thr Phe Ser Glu Tyr Pro	
395 400 405	
ccg ctt ggt aga ttt gcc gtc agg gac atg cgc cag act gtt gca gtg	1302
Pro Leu Gly Arg Phe Ala Val Arg Asp Met Arg Gln Thr Val Ala Val	
410 415 420	
gga gtc atc aag agt gtc gag aaa aag gaa cct tct gga gct aag gtg	1350
Gly Val Ile Lys Ser Val Glu Lys Lys Glu Pro Ser Gly Ala Lys Val	
425 430 435	
act aaa tct gct gcc aag aag ggt ggc aaa tgaaccgtgc aagtcagagt	1400
Thr Lys Ser Ala Ala Lys Lys Gly Gly Lys	
440 445	

tgaigtatgaat gaaggctatt ggaagaataa agactgggcc ctggtagcg gtctaattat 1460  
 tggatgtca gcagttgggt tggagaacta cagtttcaat tcagcgccat caicacggag 1520  
 ctgtgttcc cagaattggg ttcttgaccg tgggtggcat tggctgttgg ttgagtgac 1580  
 ttctttgtgt catgtttaga ctttatcgga ttgtctatt cataaagcgg ctggggaatt 1640  
 ttaaaaaaaaa aaaaaaaaaa aaaa 1664

<210> 12

<211> 449

<212> PRT

<213> Bruguiera sexangula

<400> 12

Met Gly Lys Glu Lys Ile His Ile Asn Ile Val Val Ile Gly His Val  
           1                  5                  10                  15

Asp Ser Gly Lys Ser Thr Thr Thr Gly His Leu Ile Tyr Lys Leu Gly  
                   20                  25                  30

Gly Ile Asp Lys Arg Val Ile Glu Arg Phe Glu Lys Glu Ala Ala Glu  
           35                  40                  45

Met Asn Lys Arg Ser Phe Lys Tyr Ala Trp Val Leu Asp Lys Leu Lys  
           50                  55                  60

Ala Glu Arg Glu Arg Gly Ile Thr Ile Asp Ile Ala Leu Trp Lys Phe  
           65                  70                  75                  80

Glu Thr Thr Lys Tyr Tyr Cys Thr Val Ile Asp Ala Pro Gly His Arg  
                   85                  90                  95

Asp Phe Ile Lys Asn Met Ile Thr Gly Thr Ser Gln Ala Asp Cys Ala  
           100                  105                  110

Val Leu Ile Ile Asp Ser Thr Thr Gly Gly Phe Glu Ala Gly Ile Ser  
           115                  120                  125

Lys Asp Gly Gln Thr Arg Glu His Ala Leu Leu Ala Phe Thr Leu Gly  
           130                  135                  140

Val Lys Gln Met Ile Cys Cys Cys Asn Lys Met Asp Ala Thr Thr Ser

145		150		155		160
Lys Tyr Ser Lys Ala Arg Tyr Asp Glu Ile Val Lys Glu Val Ser Ser						
	165		170		175	
Tyr Leu Lys Lys Val Gly Tyr Asn Pro Glu Lys Ile Pro Phe Val Pro						
	180		185		190	
Ile Ser Gly Phe Glu Gly Asp Asn Met Ile Glu Arg Ser Thr Asn Leu						
	195		200		205	
Asp Trp Tyr Lys Gly Pro Thr Leu Leu Glu Ala Leu Asp Met Ile Gln						
	210		215		220	
Glu Pro Lys Arg Pro Ser Asp Lys Pro Leu Arg Leu Pro Leu Gln Asp						
	225		230		235	240
Val Tyr Lys Ile Gly Gly Ile Gly Thr Val Pro Val Gly Arg Val Glu						
	245		250		255	
Thr Gly Val Leu Lys Pro Gly Met Val Val Thr Phe Gly Pro Ser Gly						
	260		265		270	
Leu Thr Thr Glu Val Lys Ser Val Glu Met His His Glu Ala Leu Gln						
	275		280		285	
Glu Ala Leu Pro Gly Asp Asn Val Gly Phe Asn Val Lys Asn Val Ser						
	290		295		300	
Val Lys Asp Leu Lys Arg Gly Tyr Val Ala Ser Asn Ser Lys Asp Asp						
	305		310		315	320
Pro Ala Lys Glu Ala Ser Ser Phe Thr Ser Gln Val Ile Ile Met Asn						
	325		330		335	
His Pro Gly Gln Ile Gly Asn Gly Tyr Ala Pro Val Leu Asp Cys His						
	340		345		350	
Thr Ser His Ile Ala Val Lys Phe Ser Glu Ile Leu Thr Lys Ile Asp						
	355		360		365	
Arg Arg Ser Gly Lys Glu Leu Glu Lys Glu Pro Lys Phe Leu Lys Asn						
	370		375		380	
Gly Asp Ala Gly Phe Val Lys Met Ile Pro Thr Lys Pro Met Val Val						
	385		390		395	400

Glu Thr Phe Ser Glu Tyr Pro Pro Leu Gly Arg Phe Ala Val Arg Asp  
 405 410 415

Met Arg Gln Thr Val Ala Val Gly Val Ile Lys Ser Val Glu Lys Lys  
 420 425 430

Glu Pro Ser Gly Ala Lys Val Thr Lys Ser Ala Ala Lys Lys Gly Gly  
 435 440 445

Lys

<210> 13

<211> 770

<212> DNA

<213> *Bruguiera sexangula*

<220>

<221> CDS

<222> (2).. (769)

<400> 13

c gat gat atg gac gag gcc aca ccc acc ttt gtt tgg ggc acc aat atc 49  
 Asp Asp Met Asp Glu Ala Thr Pro Thr Phe Val Trp Gly Thr Asn Ile  
 1 5 10 15

agc glg cag gat gtc aag gcc gct att cag atg ttt ttg aag cac ttc 97  
 Ser Val Gln Asp Val Lys Ala Ala Ile Gln Met Phe Leu Lys His Phe  
 20 25 30

agg gat agt aat cag agt caa agg aac gag att ttt gaa gaa ggg aag 145  
 Arg Asp Ser Asn Gln Ser Gln Arg Asn Glu Ile Phe Glu Glu Gly Lys  
 35 40 45

tac gtg aaa gcg ata cat aag gtt ctt gaa gtt gaa gga gag tcg ctt 193  
 Tyr Val Lys Ala Ile His Lys Val Leu Glu Val Glu Gly Glu Ser Leu  
 50 55 60

gat gtt gat gct cgt gat gtg ttt gat tat gat tct gat ttg tat gcc 241  
 Asp Val Asp Ala Arg Asp Val Phe Asp Tyr Asp Ser Asp Leu Tyr Ala  
 65 70 75 80

aag atg att cgg tac cca ctt gag gtt ttg gcc att ttc gac att gtt 289

Lys Met Ile Arg Tyr Pro Leu Glu Val Leu Ala Ile Phe Asp Ile Val  
                                     85                                    90                                    95

ttg atg gat att gtg agt ttg atc aac cct ttg ttt gag aaa cal gta 337  
 Leu Met Asp Ile Val Ser Leu Ile Asn Pro Leu Phe Glu Lys His Val  
                                     100                                    105                                    110

caa gtc agg att ttc aat ctt aag acc tgc att aca atg aga aat ctc 385  
 Gln Val Arg Ile Phe Asn Leu Lys Thr Ser Ile Thr Met Arg Asn Leu  
                                     115                                    120                                    125

aac cct tct gat atc gaa aag atg gtg tca ttg aag gga atg ala att 433  
 Asn Pro Ser Asp Ile Glu Lys Met Val Ser Leu Lys Gly Met Ile Ile  
                                     130                                    135                                    140

cgg tgt agt tcc ata ala ccg gag atc agg gaa gca gla ttt aga tgc 481  
 Arg Cys Ser Ser Ile Ile Pro Glu Ile Arg Glu Ala Val Phe Arg Cys  
                                     145                                    150                                    155                                    160

ctt gtt tgt ggc tac ttc tct gat ccc atc gtt gtg gat aga gga cgg 529  
 Leu Val Cys Gly Tyr Phe Ser Asp Pro Ile Val Val Asp Arg Gly Arg  
                                     165                                    170                                    175

ata agt gaa cct aaa gca tgc ttg aaa gag gaa tgt ctt act aag aac 577  
 Ile Ser Glu Pro Lys Ala Cys Leu Lys Glu Glu Cys Leu Thr Lys Asn  
                                     180                                    185                                    190

tcc atg aca cta gtt cac aat cgt tgc agg ttt gct gat aag cag att 625  
 Ser Met Thr Leu Val His Asn Arg Cys Arg Phe Ala Asp Lys Gln Ile  
                                     195                                    200                                    205

gtg agg ctc cag gag aca cct gac gag atc cct gaa gga gga aca cca 673  
 Val Arg Leu Gln Glu Thr Pro Asp Glu Ile Pro Glu Gly Gly Thr Pro  
                                     210                                    215                                    220

cac acg gtg agc tia ttg atg cal gac aag ctg gta gat gct gga aag 721  
 His Thr Val Ser Leu Leu Met His Asp Lys Leu Val Asp Ala Gly Lys  
                                     225                                    230                                    235                                    240

cca ggt gac agg gtt gag gtc act gga att tat agg gct atg agt gtt a 770  
 Pro Gly Asp Arg Val Glu Val Thr Gly Ile Tyr Arg Ala Met Ser Val  
                                     245                                    250                                    255

&lt;210&gt; 14

&lt;211&gt; 256

&lt;212&gt; PRT

<213> *Bruguiera sexangula*

&lt;400&gt; 14

Asp	Asp	Met	Asp	Glu	Ala	Thr	Pro	Thr	Phe	Val	Trp	Gly	Thr	Asn	Ile
1				5					10					15	
Ser	Val	Gln	Asp	Val	Lys	Ala	Ala	Ile	Gln	Met	Phe	Leu	Lys	His	Phe
		20						25					30		
Arg	Asp	Ser	Asn	Gln	Ser	Gln	Arg	Asn	Glu	Ile	Phe	Glu	Glu	Gly	Lys
		35					40					45			
Tyr	Val	Lys	Ala	Ile	His	Lys	Val	Leu	Glu	Val	Glu	Gly	Glu	Ser	Leu
	50					55					60				
Asp	Val	Asp	Ala	Arg	Asp	Val	Phe	Asp	Tyr	Asp	Ser	Asp	Leu	Tyr	Ala
65					70				75						80
Lys	Met	Ile	Arg	Tyr	Pro	Leu	Glu	Val	Leu	Ala	Ile	Phe	Asp	Ile	Val
			85						90					95	
Leu	Met	Asp	Ile	Val	Ser	Leu	Ile	Asn	Pro	Leu	Phe	Glu	Lys	His	Val
		100						105					110		
Gln	Val	Arg	Ile	Phe	Asn	Leu	Lys	Thr	Ser	Ile	Thr	Met	Arg	Asn	Leu
		115					120					125			
Asn	Pro	Ser	Asp	Ile	Glu	Lys	Met	Val	Ser	Leu	Lys	Gly	Met	Ile	Ile
	130					135					140				
Arg	Cys	Ser	Ser	Ile	Ile	Pro	Glu	Ile	Arg	Glu	Ala	Val	Phe	Arg	Cys
145				150					155						160
Leu	Val	Cys	Gly	Tyr	Phe	Ser	Asp	Pro	Ile	Val	Val	Asp	Arg	Gly	Arg
			165					170					175		
Ile	Ser	Glu	Pro	Lys	Ala	Cys	Leu	Lys	Glu	Glu	Cys	Leu	Thr	Lys	Asn
		180					185					190			
Ser	Met	Thr	Leu	Val	His	Asn	Arg	Cys	Arg	Phe	Ala	Asp	Lys	Gln	Ile
	195						200					205			
Val	Arg	Leu	Gln	Glu	Thr	Pro	Asp	Glu	Ile	Pro	Glu	Gly	Gly	Thr	Pro
	210					215					220				

His Thr Val Ser Leu Leu Met His Asp Lys Leu Val Asp Ala Gly Lys  
 225 230 235 240

Pro Gly Asp Arg Val Glu Val Thr Gly Ile Tyr Arg Ala Met Ser Val  
 245 250 255

<210> 15

<211> 846

<212> DNA

<213> Mesembryanthemum crystallinum

<220>

<221> CDS

<222> (39).. (530)

<400> 15

caaattttct ttgc tgaatc gaatctacaa aatacctg atg ggt cag gtt ctt gac 56  
 Met Gly Gln Val Leu Asp  
 1 5

aaa ttt caa cgt aag caa tgg aga caa aag caa atc cag aag ata aca 104  
 Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys Gln Ile Gln Lys Ile Thr  
 10 15 20

gat aag gta ttt gat cgt gtc aaa agt ccg acc gga aat ggc act ctt 152  
 Asp Lys Val Phe Asp Arg Val Lys Ser Pro Thr Gly Asn Gly Thr Leu  
 25 30 35

aca ttt gaa gag ctg tat ata gct acc ctg att gtc tac aat gat ala 200  
 Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu Ile Val Tyr Asn Asp Ile  
 40 45 50

aac aag tat ttg ccg ggg ccg cac ttt gat cct cca tcg aaa gac aaa 248  
 Asn Lys Tyr Leu Pro Gly Pro His Phe Asp Pro Pro Ser Lys Asp Lys  
 55 60 65 70

atc aga gcc ttg atg cag gaa tgc gat atg gat gtc gat gga gaa ctt 296  
 Ile Arg Ala Leu Met Gln Glu Cys Asp Met Asp Val Asp Gly Glu Leu  
 75 80 85

aac cgt gag gaa ttt gtg aag ttc atg cag aag glg aca gcc gat aca 344  
 Asn Arg Glu Glu Phe Val Lys Phe Met Gln Lys Val Thr Ala Asp Thr  
 90 95 100



ttc tct acg gtc agc cag gga ctg att atc tct ctg att ctg gcg cca 392  
 Phe Ser Thr Val Ser Gln Gly Leu Ile Ile Ser Leu Ile Leu Ala Pro  
 105 110 115  
 aca gtt gca ttg gcg acg aag agg gca aca gaa ggt gtt cca ggt gtg 440  
 Thr Val Ala Leu Ala Thr Lys Arg Ala Thr Glu Gly Val Pro Gly Val  
 120 125 130  
 ggg aaa gtg gtg caa aag gtg cct act tca att tat gca tcc ctg gtg 488  
 Gly Lys Val Val Gln Lys Val Pro Thr Ser Ile Tyr Ala Ser Leu Val  
 135 140 145 150  
 acc ctt gtt gtc gtt gca atc caa act gct agc gag gga tgc 530  
 Thr Leu Val Val Val Ala Ile Gln Thr Ala Ser Glu Gly Cys  
 155 160  
 tgallagagg ctttagttac ttgttcatga tacagaagga acagttcttg tcaattttatt 590  
 tcttttttaa taggacataa ggaagttgta taictttctt ctttcttcta ccaggttttg 650  
 .ggggaagttg gaaagaacat acaaatgatt tcaactgcgt attggctgat cctcccaattt 710  
 attaaaaactt gtcgtgtcta gcatgagcga ttcaataattt gcaataatgca atatttgtaa 770  
 tgaigtctac attcagtgat tagtgtgatt gtgcagtttg ttgggaaaaa aaaaaaaaaa 830  
 aaaaaaaaaa aaaaaa 846

&lt;210&gt; 16

&lt;211&gt; 164

&lt;212&gt; PRT

&lt;213&gt; Mesembryanthemum crystallinum

&lt;400&gt; 16

Met Gly Gln Val Leu Asp Lys Phe Gln Arg Lys Gln Trp Arg Gln Lys

1

5

10

15

Gln Ile Gln Lys Ile Thr Asp Lys Val Phe Asp Arg Val Lys Ser Pro

20

25

30

Thr Gly Asn Gly Thr Leu Thr Phe Glu Glu Leu Tyr Ile Ala Thr Leu

35

40

45

Ile Val Tyr Asn Asp Ile Asn Lys Tyr Leu Pro Gly Pro His Phe Asp

50

55

60

Pro Pro Ser Lys Asp Lys Ile Arg Ala Leu Met Gln Glu Cys Asp Met  
 65 70 75 80  
 Asp Val Asp Gly Glu Leu Asn Arg Glu Glu Phe Val Lys Phe Met Gln  
 85 90 95  
 Lys Val Thr Ala Asp Thr Phe Ser Thr Val Ser Gln Gly Leu Ile Ile  
 100 105 110  
 Ser Leu Ile Leu Ala Pro Thr Val Ala Leu Ala Thr Lys Arg Ala Thr  
 115 120 125  
 Glu Gly Val Pro Gly Val Gly Lys Val Val Gln Lys Val Pro Thr Ser  
 130 135 140  
 Ile Tyr Ala Ser Leu Val Thr Leu Val Val Val Ala Ile Gln Thr Ala  
 145 150 155 160  
 Ser Glu Gly Cys

&lt;210&gt; 17

&lt;211&gt; 872

&lt;212&gt; DNA

&lt;213&gt; Mesembryanthemum crystallinum

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (183)..(569)

&lt;400&gt; 17

aacaaaatgt ctcctctttt cctttctctt ttctctttct ctcctttcgt gggttgattg 60

agtaagctct gtccttttgc tctctgttga atgtactalc ttctgtgaac caaaggccaa 120

agattaacta ttggagattt cctactcga aatttgtttt taggtgttga cccgtttgag 180

ct atg gcg aac aag ccc caa att cca acg aag aat tcg gcc ctc att 227

Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile

1

5

10

15

gct att atc gcg gat gag gat act gta act gga ttt ttg ctg gct gga 275

Ala Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly

	20	25	30	
ggt ggt aat gtt gat cta cga aga cag aca aat tac att att gtt gac				323
Val Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp				
	35	40	45	
aat aaa aca acg atg aag caa atc gaa gat gca ttc aag gag ttc aca				371
Asn Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr				
	50	55	60	
gca aga gag gac att gcg gtt gta cta atc agc caa tat gtt gca aat				419
Ala Arg Glu Asp Ile Ala Val Val Leu Ile Ser Gln Tyr Val Ala Asn				
	65	70	75	
atg ata aga gta ttg gtt gat agc tac aac aaa cca atc ccg gca att				467
Met Ile Arg Val Leu Val Asp Ser Tyr Asn Lys Pro Ile Pro Ala Ile				
	80	85	90	95
ttg gag att cct tca aag gac cat cct tat gat cct aac cat gat tca				515
Leu Glu Ile Pro Ser Lys Asp His Pro Tyr Asp Pro Asn His Asp Ser				
	100	105	110	
gtc ctt tca agg gtt aaa tac ctg ttc tct tct gaa tgg gca tca agc				563
Val Leu Ser Arg Val Lys Tyr Leu Phe Ser Ser Glu Ser Ala Ser Ser				
	115	120	125	
aga ttt tagccataag ctttgtaaag ttccctgcct ctgaatgttt ggtgattatg				619
Arg Phe				
agtttaaaact agaaccagtc acattcigac ttggtatttt gaggcacigt ttgttttatg				679
ttcttlaaaat aaggagtgta attacgacac catgaatcgg galatgacac catgaatcgc				739
atgtatttct ttccatctca ttgaaagag tggagcagcc atatcattta gtctcttct				799
cttgcgaatg agcttgggaag aaatgttttg gctataaaaag atttcaactc ttggtacaaa				859
aaaaaaaaaa aaa				872

&lt;210&gt; 18

&lt;211&gt; 129

&lt;212&gt; PRT

&lt;213&gt; Mesembryanthemum crystallinum

&lt;400&gt; 18

Met Ala Asn Lys Pro Gln Ile Pro Thr Lys Asn Ser Ala Leu Ile Ala  
 1 5 10 15

Ile Ile Ala Asp Glu Asp Thr Val Thr Gly Phe Leu Leu Ala Gly Val  
 20 25 30

Gly Asn Val Asp Leu Arg Arg Gln Thr Asn Tyr Ile Ile Val Asp Asn  
 35 40 45

Lys Thr Thr Met Lys Gln Ile Glu Asp Ala Phe Lys Glu Phe Thr Ala  
 50 55 60

Arg Glu Asp Ile Ala Val Val Leu Ile Ser Gln Tyr Val Ala Asn Met  
 65 70 75 80

Ile Arg Val Leu Val Asp Ser Tyr Asn Lys Pro Ile Pro Ala Ile Leu  
 85 90 95

Glu Ile Pro Ser Lys Asp His Pro Tyr Asp Pro Asn His Asp Ser Val  
 100 105 110

Leu Ser Arg Val Lys Tyr Leu Phe Ser Ser Glu Ser Ala Ser Ser Arg  
 115 120 125

Phe

<210> 19

<211> 647

<212> DNA

<213> Mesembryanthemum crystallinum

<220>

<221> CDS

<222> (64).. (426)

<400> 19

cttgttttct tctctccctt ctcctctctt tctccgcacc ctcaggcagt gaaggttagca 60

aca atg gcg tac gcg atg aag cca acg aag ccc ggg atg gag gaa tcc 108  
 Met Ala Tyr Ala Met Lys Pro Thr Lys Pro Gly Met Glu Glu Ser  
 1 5 10 15

cag gag cag att cac aag atc agg atc act ctt tct tct aag aac gtc 156

Gln Glu Gln Ile His Lys Ile Arg Ile Thr Leu Ser Ser Lys Asn Val  
 20 25 30  
 aag aac ctt gag aaa gtg tgt gct gat ctt gta cgc ggt gca aag gac 204  
 Lys Asn Leu Glu Lys Val Cys Ala Asp Leu Val Arg Gly Ala Lys Asp  
 35 40 45  
 aag cgc ctc agg gtt aag gga cca gtg agg atg ccc acc aag gtt ctg 252  
 Lys Arg Leu Arg Val Lys Gly Pro Val Arg Met Pro Thr Lys Val Leu  
 50 55 60  
 aag atc aca aca agg aag tct ccc tgt ggt gaa gga acc aac acc ttt 300  
 Lys Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly Thr Asn Thr Phe  
 65 70 75  
 gac aga ttt gag ttg cgt gtt cac aag aga gtc att gac ctc ttc agc 348  
 Asp Arg Phe Glu Leu Arg Val His Lys Arg Val Ile Asp Leu Phe Ser  
 80 85 90 95  
 tcc cca gac gtg gtc aag cag atc acc tcc atc acc att gaa cct ggt 396  
 Ser Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr Ile Glu Pro Gly  
 100 105 110  
 gtt gag gtt gag gtt aca ata gct gac tct tagacatgcc tgttgaagtt 446  
 Val Glu Val Glu Val Thr Ile Ala Asp Ser  
 115 120  
 gtctgtctgtg tagggcgttt gtagctgtct catatagttg tgcatactca ctaagaattt 506  
 tgaagalact aaattgtttg ttgaaagag atgttttctt tagctgtaat gttatgtttt 566  
 tgaaggigtgtt ggaacatgca ttatttgita atgctttatc aatagaactt ccaatttgaa 626  
 tgcaaaaaaa aaaaaaaaaa a 647

&lt;210&gt; 20

&lt;211&gt; 121

&lt;212&gt; PRT

&lt;213&gt; Mesembryanthemum crystallinum

&lt;400&gt; 20

Met Ala Tyr Ala Met Lys Pro Thr Lys Pro Gly Met Glu Glu Ser Gln  
 1 5 10 15

Glu Gln Ile His Lys Ile Arg Ile Thr Leu Ser Ser Lys Asn Val Lys

20	25	30
Asn Leu Glu Lys Val Cys Ala Asp Leu Val Arg Gly Ala Lys Asp Lys		
35	40	45
Arg Leu Arg Val Lys Gly Pro Val Arg Met Pro Thr Lys Val Leu Lys		
50	55	60
Ile Thr Thr Arg Lys Ser Pro Cys Gly Glu Gly Thr Asn Thr Phe Asp		
65	70	75
		80
Arg Phe Glu Leu Arg Val His Lys Arg Val Ile Asp Leu Phe Ser Ser		
85	90	95
Pro Asp Val Val Lys Gln Ile Thr Ser Ile Thr Ile Glu Pro Gly Val		
100	105	110
Glu Val Glu Val Thr Ile Ala Asp Ser		
115	120	

<210> 21  
 <211> 686  
 <212> DNA  
 <213> Sueada japonica

<220>  
 <221> CDS  
 <222> (62).. (493)

<400> 21  
 acaccattca caaaacacat taataaaaaaa cactacttct ttctttcttta gccacttgaa 60

a atg gcc tac tca aag gct gta ctc ctt gcc ctt atc ttt gct gtg act 109  
 Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr  
 1 5 10 15

ctt gtc att gcc tct cag gtc tca gct cgt gaa ctt gct gag gag aca 157  
 Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr  
 20 25 30

caa tct gtg gag gag tct aag gga tac ggt ggt ggg cac gga ggt cac 205  
 Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly Gly His Gly Gly His  
 35 40 45

tat ggt ggt ggt cac tat ggt ggt gga cac aga cac ggt ggc cat gga 253  
 Tyr Gly Gly Gly His Tyr Gly Gly Gly His Arg His Gly Gly His Gly  
           50                          55                          60

cac tac gca act gag gaa gca gag aac aag aat gaa gcc gta gaa cct 301  
 His Tyr Ala Thr Glu Glu Ala Glu Asn Lys Asn Glu Ala Val Glu Pro  
           65                          70                          75                          80

caa ggc ggc tat ggt cac gga cac gga gga ggc tac gga cac ggt ggt 349  
 Gln Gly Gly Tyr Gly His Gly His Gly Gly Gly Tyr Gly His Gly Gly  
                                   85                                  90                                  95

ggc tac gga cac ggt gga ggc tac gga cac gga ggt ggc tac ggc cac 397  
 Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His  
                           100                          105                          110

ggt ggt ggc tac gga cat gga ggt ggt tat gga cac ggt gga cac ggt 445  
 Gly Gly Gly Tyr Gly His Gly Gly Gly Tyr Gly His Gly Gly His Gly  
           115                          120                          125

gga cat ggt ggt cat ggt cac tac gcc aag act acc gag gaa caa aat 493  
 Gly His Gly Gly His Gly His Tyr Ala Lys Thr Thr Glu Glu Gln Asn  
           130                          135                          140

taagttaagg gttactaaaa cttaaatgtt acgttgtcaa ataaaatgta cttaatgatt 553

ttacatgagt atgcatgtaa ttcatcataa gcttcaagga ctatcttgta ctctatgtta 613

tataacctata tgaatggaa gcgtgacttt tattactgta aaaaaaaaaa aaaaaaaaaa 673

aaaaaaaaaa aaa 686

<210> 22

<211> 144

<212> PRT

<213> Sueada japonica

<400> 22

Met Ala Tyr Ser Lys Ala Val Leu Leu Ala Leu Ile Phe Ala Val Thr  
           1                          5                          10                          15

Leu Val Ile Ala Ser Gln Val Ser Ala Arg Glu Leu Ala Glu Glu Thr  
                           20                          25                          30

Gln Ser Val Glu Glu Ser Lys Gly Tyr Gly Gly Gly His Gly Gly His

<400> 23																	
gttaa	gatat	tatat	tgcaa	cttt	acaaag	cattt	cttgca	actaa	aal	alg	gcc	ttt				56	
											Met	Ala	Phe				
											1						
tcc	aaa	cc	t	cia	att	gct	tct	cia	ctt	ctt	tct	cic	ttt	gtt	ctt	cag	104
Ser	Lys	Pro	Leu	Ile	Ala	Ser	Leu	Leu	Leu	Ser	Leu	Phe	Val	Leu	Gln		
	5					10					15						
ttt	gtt	cat	gca	gtt	gaa	cc	t	att	tca	tcc	tcc	aat	caa	gtg	ggt	agc	152
Phe	Val	His	Ala	Val	Glu	Pro	Ile	Ser	Ser	Ser	Asn	Gln	Val	Gly	Ser		
20					25					30					35		
aac	act	gga	ggt	acc	tca	gag	agt	aaa	gig	gat	tgt	ggg	gcg	gca	tgt		200
Asn	Thr	Gly	Gly	Thr	Ser	Glu	Ser	Lys	Val	Asp	Cys	Gly	Ala	Ala	Cys		



40 45 50  
 acg gtg agg tgc agc gcc tgc aag agg cca aac cta tgc aac agg tca 248  
 Thr Val Arg Cys Ser Ala Ser Lys Arg Pro Asn Leu Cys Asn Arg Ser  
 55 60 65  
 tgt ggc agt tgt tgc aag acg tgc aac tgc gtg cca cca ggc act tcc 296  
 Cys Gly Ser Cys Cys Lys Thr Cys Asn Cys Val Pro Pro Gly Thr Ser  
 70 75 80  
 ggc aac tac gaa gcc tgc cct tgt tac gcc aac ttg acc acc cac ggc 344  
 Gly Asn Tyr Glu Ala Cys Pro Cys Tyr Ala Asn Leu Thr Thr His Gly  
 85 90 95  
 aat cga cac aag tgc cct taattaacaa gaattgttta gtgtttatt 392  
 Asn Arg His Lys Cys Pro  
 100 105  
 acatccgtac catgtaacgt acicciattt acaciactag aglactagta ataaacattt 452  
 ttaggcacgg tccagttgtt catgtagcta giggtatatt gagicataaa tgagtgtttg 512  
 aaaatgagat atgataaaag tgtattatct acattgtagt actgttttgt atcatagtgt 572  
 agtgatgttt atttttctga cctttaattt gttactttgt attccctttc attctaicta 632  
 tttaaatcc ttttgtlaagt ttatgtgaaa aaaaaaaaaa aaaaaaaaaa a 683

&lt;210&gt; 24

&lt;211&gt; 105

&lt;212&gt; PRT

&lt;213&gt; Salsola komarovii

&lt;400&gt; 24

Met Ala Phe Ser Lys Pro Leu Ile Ala Ser Leu Leu Leu Ser Leu Phe

1

5

10

15

Val Leu Gln Phe Val His Ala Val Glu Pro Ile Ser Ser Ser Asn Gln

20

25

30

Val Gly Ser Asn Thr Gly Gly Thr Ser Glu Ser Lys Val Asp Cys Gly

35

40

45

Ala Ala Cys Thr Val Arg Cys Ser Ala Ser Lys Arg Pro Asn Leu Cys

50

55

60

Asn Arg Ser Cys Gly Ser Cys Cys Lys Thr Cys Asn Cys Val Pro Pro  
 65 70 75 80  
 Gly Thr Ser Gly Asn Tyr Glu Ala Cys Pro Cys Tyr Ala Asn Leu Thr  
 85 90 95  
 Thr His Gly Asn Arg His Lys Cys Pro  
 100 105

<210> 25  
 <211> 803  
 <212> DNA  
 <213> Salsola komarovii

<220>  
 <221> CDS  
 <222> (51)..(593)

<400> 25  
 cgcagacgct tcagctcttt ctcctctctt ctcctctctc accgtgaaag atg ggg 56  
 Met Gly  
 1  
 ttg tca ttt acc aaa ttg ttt agc cgg ttg ttc gct aag aag gaa atg 104  
 Leu Ser Phe Thr Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys Glu Met  
 5 10 15  
 cgt atc ctt atg gtc ggt ctc gat gcc gct ggt aaa acc acc att ctc 152  
 Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr Ile Leu  
 20 25 30  
 tat aaa ctc aag ctg gga gag att gtc acc acc att cct acc att gga 200  
 Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr Ile Gly  
 35 40 45 50  
 ttt aat gtg gag act gta gaa tac aag aac atc agc ttc act gtg tgg 248  
 Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr Val Trp  
 55 60 65  
 gat gtc ggg ggt caa gac aag att cgt cca ttg tgg aga cat tac ttc 296  
 Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His Tyr Phe  
 70 75 80

caa aac acc caa ggt ctc atc ttt gtg gtt gac agt aat gat cgt gac 344  
 Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp Arg Asp  
                   85                                  90                                  95

cgt gtc gtt gag gca aga gat gaa ctg cat agg atg tta aat gag gat 392  
 Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn Glu Asp  
           100                                  105                                  110

gaa tta cga gat gca gtg ttg ttg gtg ttt gca aac aag caa gat ctt 440  
 Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln Asp Leu  
           115                                  120                                  125                                  130

ccc aat gca atg aat gct gct gag atc act gat aag ctt ggt ctc cat 488  
 Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly Leu His  
                                   135                                  140                                  145

tct cta cgt caa cgc cat tgg tac ata caa agc aca tgt gcc acc tct 536  
 Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala Thr Ser  
                                   150                                  155                                  160

gga gaa ggg ctt tac gag ggt ctg gac tgg ctc tca aac aat atc gct 584  
 Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn Ile Ala  
                                   165                                  170                                  175

agc aag gct taaaagtaac agaacgagta aggttagctt tctcagagaa 633  
 Ser Lys Ala  
                   180

gaagctggag tataggciga ggactatcgt tactgctagt gtlacccttt ttatttttgc 693

catttataig ttacattttt tggltcctat cggacaagaa ttattttctg cgttttatgtt 753

gacttgttat aataccatac ttttttagttg aaaaaaaaaa aaaaaaaaaa 803

<210> 26

<211> 181

<212> PRT

<213> Salsola komarovii

<400> 26

Met Gly Leu Ser Phe Thr Lys Leu Phe Ser Arg Leu Phe Ala Lys Lys  
           1                                  5                                  10                                  15

Glu Met Arg Ile Leu Met Val Gly Leu Asp Ala Ala Gly Lys Thr Thr  
                   20                                  25                                  30

Ile Leu Tyr Lys Leu Lys Leu Gly Glu Ile Val Thr Thr Ile Pro Thr  
                   35                                  40                                  45  
 Ile Gly Phe Asn Val Glu Thr Val Glu Tyr Lys Asn Ile Ser Phe Thr  
           50                                  55                                  60  
 Val Trp Asp Val Gly Gly Gln Asp Lys Ile Arg Pro Leu Trp Arg His  
       65                                  70                                  75                                  80  
 Tyr Phe Gln Asn Thr Gln Gly Leu Ile Phe Val Val Asp Ser Asn Asp  
                                   85                                  90                                  95  
 Arg Asp Arg Val Val Glu Ala Arg Asp Glu Leu His Arg Met Leu Asn  
                                   100                                  105                                  110  
 Glu Asp Glu Leu Arg Asp Ala Val Leu Leu Val Phe Ala Asn Lys Gln  
           115                                  120                                  125  
 Asp Leu Pro Asn Ala Met Asn Ala Ala Glu Ile Thr Asp Lys Leu Gly  
       130                                  135                                  140  
 Leu His Ser Leu Arg Gln Arg His Trp Tyr Ile Gln Ser Thr Cys Ala  
       145                                  150                                  155                                  160  
 Thr Ser Gly Glu Gly Leu Tyr Glu Gly Leu Asp Trp Leu Ser Asn Asn  
                                   165                                  170                                  175  
 Ile Ala Ser Lys Ala  
                                   180

<210> 27

<211> 680

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (161)..(454)

<400> 27

ctaaaagcca aaggcaagat aagaacagg ttccctttagc tatcttccctc gtcctgcctgc 60

tgcaaaagtt ccatccccag aagatcagga aaaccttctc gcagcagcac tctaataatc 120

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ctccaatttt gatccaagag aagaaacaaa ataaacagaa atg gct cgc tct ttc 175
                               Met Ala Arg Ser Phe
                               1           5

tcc aac gct aag acc gtc tct gct gtc att gcc aac gaa atc tca gct 223
Ser Asn Ala Lys Thr Val Ser Ala Val Ile Ala Asn Glu Ile Ser Ala
          10           15           20

ctt gtc acc agg agg ggt tat gct gct ctc gca cag ggc gtt gtt tgc 271
Leu Val Thr Arg Arg Gly Tyr Ala Ala Leu Ala Gln Gly Val Val Ser
          25           30           35

agc agc gcg aga agc ggc ggc gct ccg aac gtg atg ctg aag aaa gga 319
Ser Ser Ala Arg Ser Gly Gly Ala Pro Asn Val Met Leu Lys Lys Gly
          40           45           50

tcc gaa gaa tcc ggg aag aca gca tgg glg ccc gac ccg gac acc ggc 367
Ser Glu Glu Ser Gly Lys Thr Ala Trp Val Pro Asp Pro Asp Thr Gly
          55           60           65

tac tac cga ccg gga aac gag gac aag gcc gcg ctg gac ccg gtc gag 415
Tyr Tyr Arg Pro Gly Asn Glu Asp Lys Ala Ala Leu Asp Pro Val Glu
          70           75           80           85

ctg cgg gag atg ctc atc aag aac aag ccc agc cga caa tgaatgaacc 464
Leu Arg Glu Met Leu Ile Lys Asn Lys Pro Ser Arg Gln
          90           95

aagaattgtg ggattctcat taattcctcc ccgttctgg tccatcgtcg gaatctgaac 524

ctgttgttcg tctagaaatt cgtlcccatg gaaatctatc aaagtctgta ttcttgccat 584

ggctcttccct glcccatata tgtatgtcct cagggtgtggc ctgggggtggt ttgatagata 644

tataaaatgt ggtgaattta aaaaaaaaaa aaaaaa 680

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&lt;210&gt; 28

&lt;211&gt; 98

&lt;212&gt; PRT

&lt;213&gt; Avicennia marina

&lt;400&gt; 28

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Met Ala Arg Ser Phe Ser Asn Ala Lys Thr Val Ser Ala Val Ile Ala
 1           5           10           15

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Asn Glu Ile Ser Ala Leu Val Thr Arg Arg Gly Tyr Ala Ala Leu Ala  
                     20                    25                    30  
 Gln Gly Val Val Ser Ser Ser Ala Arg Ser Gly Gly Ala Pro Asn Val  
                     35                    40                    45  
 Met Leu Lys Lys Gly Ser Glu Glu Ser Gly Lys Thr Ala Trp Val Pro  
                     50                    55                    60  
 Asp Pro Asp Thr Gly Tyr Tyr Arg Pro Gly Asn Glu Asp Lys Ala Ala  
                     65                    70                    75                    80  
 Leu Asp Pro Val Glu Leu Arg Glu Met Leu Ile Lys Asn Lys Pro Ser  
                     85                    90                    95  
 Arg Gln

<210> 29  
 <211> 490  
 <212> DNA  
 <213> *Avicennia marina*

<220>  
 <221> CDS  
 <222> (20).. (349)

<400> 29  
 tcggctgggc aaagaaggg atg gcg att cca tcg gaa att cgg gac ttt att 52  
                     Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile  
                                     1                    5                    10  
 gct agc cgc aac aga tct ttg gtg atc gca tct cca aag gaa gat gag 100  
 Ala Ser Arg Asn Arg Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu  
                     15                    20                    25  
 aaa att ctc cgc tca agg cag tgc acc gaa gaa ggg gcg cgt gca gga 148  
 Lys Ile Leu Arg Ser Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly  
                     30                    35                    40  
 gcc aaa gct gct gca gtt gct tgc gtt gcc agc gcc att ccc act ctg 196  
 Ala Lys Ala Ala Ala Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu  
                     45                    50                    55

gta gcl gti cga acg att ccg tgg gca aag gca aac ctc aac tat aca 244  
 Val Ala Val Arg Thr Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr  
 60 65 70 75

gcc cag gca ctc att ata tct tct gca tcc ata gcg gca tac ttt atc 292  
 Ala Gln Ala Leu Ile Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile  
 80 85 90

gct gcl gac aaa acc atc tta gag tgc gca cgg aaa aat gca gag tac 340  
 Ala Ala Asp Lys Thr Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr  
 95 100 105

aaa tcg gct taagatgaig tgaagacaa tglgtcagc ttgcaatgct 389  
 Lys Ser Ala  
 110

tgccatgact lgtgtttatg tgtatttcaa gtctctgaaa ctgcatlitt gatlttgtgt 449

tccaatgcaa tgagcattat ggaaaaaaaa aaaaaaaaaa a 490

<210> 30

<211> 110

<212> PRT

<213> Avicennia marina

<400> 30

Met Ala Ile Pro Ser Glu Ile Arg Asp Phe Ile Ala Ser Arg Asn Arg  
 1 5 10 15

Ser Leu Val Ile Ala Ser Pro Lys Glu Asp Glu Lys Ile Leu Arg Ser  
 20 25 30

Arg Gln Cys Thr Glu Glu Gly Ala Arg Ala Gly Ala Lys Ala Ala Ala  
 35 40 45

Val Ala Cys Val Ala Ser Ala Ile Pro Thr Leu Val Ala Val Arg Thr  
 50 55 60

Ile Pro Trp Ala Lys Ala Asn Leu Asn Tyr Thr Ala Gln Ala Leu Ile  
 65 70 75 80

Ile Ser Ser Ala Ser Ile Ala Ala Tyr Phe Ile Ala Ala Asp Lys Thr  
 85 90 95

Ile Leu Glu Cys Ala Arg Lys Asn Ala Glu Tyr Lys Ser Ala  
 100 105 110

<210> 31  
 <211> 592  
 <212> DNA  
 <213> *Avicennia marina*

<220>  
 <221> CDS  
 <222> (75)..(320)

<400> 31

gcagtcacag ccttcctgct cctcgggag cticaaatit gtgaattitc cgagtgciaa 60

aagattcagc caag atg cag aac gaa gag ggg caa aac atg gat ctc tac 110  
 Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr  
 1 5 10

atc ccc agg aaa tgc tct gcc acg aac agg ctg atc acc tcc aag gat 158  
 Ile Pro Arg Lys Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp  
 15 20 25

cat gct tct gtc cag atc aat gtt ggg cac ttg gat gag aat ggc cga 206  
 His Ala Ser Val Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg  
 30 35 40

tac act ggc caa tac tct acc ttt gct ctt tgt gga ttc atc cgt gct 254  
 Tyr Thr Gly Gln Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala  
 45 50 55 60

cag ggt gat gct gac agt gct ctt gat agg ctc tgg cag aaa aag aaa 302  
 Gln Gly Asp Ala Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys  
 65 70 75

gtc gaa acc agg cag cag tgatcctgct caattcagca gtaaaagttt 350  
 Val Glu Thr Arg Gln Gln  
 80

tttgggtttt gtctctgtgt gtgttatitg tgcctttcca gaatcaattt ctgtactgga 410

ttgagtattg aaaatgtgga gctaaagggt gggagacctg atgcctttgt tactcgagta 470

atcacaagta gatactgggc ttgtaatagc gtgataatig tgccttgctc ttgcctcatt 530



gactacgaat cagitaigtg attagacaat gtaaatcicc aaaaaaaaaa aaaaaaaaaa 590

aa 592

<210> 32

<211> 82

<212> PRT

<213> Avicennia marina

<400> 32

Met Gln Asn Glu Glu Gly Gln Asn Met Asp Leu Tyr Ile Pro Arg Lys  
1 5 10 15

Cys Ser Ala Thr Asn Arg Leu Ile Thr Ser Lys Asp His Ala Ser Val  
20 25 30

Gln Ile Asn Val Gly His Leu Asp Glu Asn Gly Arg Tyr Thr Gly Gln  
35 40 45

Tyr Ser Thr Phe Ala Leu Cys Gly Phe Ile Arg Ala Gln Gly Asp Ala  
50 55 60

Asp Ser Ala Leu Asp Arg Leu Trp Gln Lys Lys Lys Val Glu Thr Arg  
65 70 75 80

Gln Gln

<210> 33

<211> 1806

<212> DNA

<213> Avicennia marina

<220>

<221> CDS

<222> (362).. (1552)

<400> 33

tgtagaaggta aagctacag catatttcgc gccgcicgtt tgattacgtg ttgcttttat 60

ttgggaattt gatagcgcig agtagccgat gccgcitggag ggtattgttg attttaggaa 120

tacgggtttg ttgattcgc agttttactg tctctagggt tgggccctga ggcttctggg 180  
 atttgggatt taatcgciga tcgaacagtt tcttggagaa aatattccia gtgcgatai 240  
 atctgatttg ctgacgagaa attgatacac ggltatgcga ttgagttttg ttgctgcca 300  
 agatactccg agtgcctgct agatgtggat aatccggagg gcgttttca tgagaigagg 360  
 g atg tta tca ggg tta atg aac ttc ctg tgg gcc tgt ttt cgg cca agg 409  
 Met Leu Ser Gly Leu Met Asn Phe Leu Trp Ala Cys Phe Arg Pro Arg  
 1 5 10 15  
 gcg gat cga agt gtt cac acg ggt tca gat gca ggc ggt cgt cag gat 457  
 Ala Asp Arg Ser Val His Thr Gly Ser Asp Ala Gly Gly Arg Gln Asp  
 20 25 30  
 ggg ctt tta tgg tat aag gac ttg ggg caa cat atc aat gga gag ttt 505  
 Gly Leu Leu Trp Tyr Lys Asp Leu Gly Gln His Ile Asn Gly Glu Phe  
 35 40 45  
 tca atg gct gla gtt caa gca aat aac tta cta gag gat cag agt caa 553  
 Ser Met Ala Val Val Gln Ala Asn Asn Leu Leu Glu Asp Gln Ser Gln  
 50 55 60  
 ctt gaa tct ggt tgc ctg agc ttg agt gat tca gga caa tat ggc act 601  
 Leu Glu Ser Gly Cys Leu Ser Leu Ser Asp Ser Gly Gln Tyr Gly Thr  
 65 70 75 80  
 ttt gtg ggg att tat gat gga cat gga ggt cct gag acc tct cgg ttt 649  
 Phe Val Gly Ile Tyr Asp Gly His Gly Gly Pro Glu Thr Ser Arg Phe  
 85 90 95  
 atc aat gac cat ctg ttc caa cat ata aag aga ttc aca gct gag cat 697  
 Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His  
 100 105 110  
 caa tca atg tca gct gag gtc att cac aag gcc att caa gcg act gaa 745  
 Gln Ser Met Ser Ala Glu Val Ile His Lys Ala Ile Gln Ala Thr Glu  
 115 120 125  
 gaa ggt ttt ttc tcg gtt gtt agc aga caa tgg tcc atg caa cca cag 793  
 Glu Gly Phe Phe Ser Val Val Ser Arg Gln Trp Ser Met Gln Pro Gln  
 130 135 140  
 att gca gca gtt ggc tct tgc tgc ctt gtt ggt gtc atc tgt agt ggc 841  
 Ile Ala Ala Val Gly Ser Cys Cys Leu Val Gly Val Ile Cys Ser Gly

145	150	155	160	
act ctt tat gtt tcc aac ctt ggt gat tcc cgt gct gtt ctt ggg acg				889
Thr Leu Tyr Val Ser Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Thr				
	165	170	175	
ctt tcc aag gct aca ggg gaa gla cag gct act caa ctc tca aca gag				937
Leu Ser Lys Ala Thr Gly Glu Val Gln Ala Thr Gln Leu Ser Thr Glu				
	180	185	190	
cat aat gca agt ttt gag tct gtg aga cgg gaa ctg cag tct ctg cac				985
His Asn Ala Ser Phe Glu Ser Val Arg Arg Glu Leu Gln Ser Leu His				
	195	200	205	
cca gat gac tca cag att gtg gtt cta aag cat aat gla tgg cga gtg				1033
Pro Asp Asp Ser Gln Ile Val Val Leu Lys His Asn Val Trp Arg Val				
	210	215	220	
aag ggt ctt ata cag atc tca aga tca att gga gat gtg tat ttg aaa				1081
Lys Gly Leu Ile Gln Ile Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys				
	225	230	235	240
aag gct gaa ttc aac agg gag cct cta tat cag aaa ttt cga ctt cgt				1129
Lys Ala Glu Phe Asn Arg Glu Pro Leu Tyr Gln Lys Phe Arg Leu Arg				
	245	250	255	
gaa gct ttc aaa aga cca att ttg agc tca gaa cca gaa act act gtg				1177
Glu Ala Phe Lys Arg Pro Ile Leu Ser Ser Glu Pro Glu Thr Thr Val				
	260	265	270	
cac cag ctg ctg cct cat gat caa ttc att atc ttc gca tca gat ggc				1225
His Gln Leu Leu Pro His Asp Gln Phe Ile Ile Phe Ala Ser Asp Gly				
	275	280	285	
ctt tgg gag cac ctt tcc aac caa gaa gca gtt gat ctt gtt cag aaa				1273
Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Asp Leu Val Gln Lys				
	290	295	300	
cat cca cac aat ggg att gct aga aga tta gta aaa gca gct ttg caa				1321
His Pro His Asn Gly Ile Ala Arg Arg Leu Val Lys Ala Ala Leu Gln				
	305	310	315	320
gag gca gca aag aaa agg gaa atg agg tac tcg gat ttg aag aaa att				1369
Glu Ala Ala Lys Lys Arg Glu Met Arg Tyr Ser Asp Leu Lys Lys Ile				
	325	330	335	

gac cgt ggg gtt cgc cgt cat ttc cat gat gac atc act gtt gtg gtg 1417  
 Asp Arg Gly Val Arg Arg His Phe His Asp Asp Ile Thr Val Val Val  
 340 345 350

gtg ttt ctt gac tca cac ctt gtg agc cgg gct agc tca gtc cgg ggc 1465  
 Val Phe Leu Asp Ser His Leu Val Ser Arg Ala Ser Ser Val Arg Gly  
 355 360 365

cca aac atc tcc gig aaa ggt ggc ggc atc agt ctg cct ccc aat gct 1513  
 Pro Asn Ile Ser Val Lys Gly Gly Gly Ile Ser Leu Pro Pro Asn Ala  
 370 375 380

ctt gca cct tgl gcc aca cca acg gag cca gtc cca aat tgalactgct 1562  
 Leu Ala Pro Cys Ala Thr Pro Thr Glu Pro Val Pro Asn  
 385 390 395

gtctcttcta atgttatctt ccgttagtcc tgtgttacta ttgttatgtg aatacaggta 1622  
 gcttcttaac ggataacagc ggcccttgaa ttctttaatc calactgliaa cttttaaccg 1682  
 gagactatta ctggcatag ttccaatgcc caagggatac atagactggg acaagccaac 1742  
 ttggcggiga caatcatcat agttaagttt tctgggcata tctttcaaaa aaaaaaaaaa 1802  
 aaaa 1806

<210> 34  
 <211> 397  
 <212> PRT  
 <213> Avicennia marina

<400> 34  
 Met Leu Ser Gly Leu Met Asn Phe Leu Trp Ala Cys Phe Arg Pro Arg  
 1 5 10 15  
 Ala Asp Arg Ser Val His Thr Gly Ser Asp Ala Gly Gly Arg Gln Asp  
 20 25 30  
 Gly Leu Leu Trp Tyr Lys Asp Leu Gly Gln His Ile Asn Gly Glu Phe  
 35 40 45  
 Ser Met Ala Val Val Gln Ala Asn Asn Leu Leu Glu Asp Gln Ser Gln  
 50 55 60  
 Leu Glu Ser Gly Cys Leu Ser Leu Ser Asp Ser Gly Gln Tyr Gly Thr

65		70		75		80
Phe Val Gly Ile Tyr Asp Gly His Gly Gly Pro Glu Thr Ser Arg Phe						
	85			90		95
Ile Asn Asp His Leu Phe Gln His Ile Lys Arg Phe Thr Ala Glu His						
	100			105		110
Gln Ser Met Ser Ala Glu Val Ile His Lys Ala Ile Gln Ala Thr Glu						
	115			120		125
Glu Gly Phe Phe Ser Val Val Ser Arg Gln Trp Ser Met Gln Pro Gln						
	130			135		140
Ile Ala Ala Val Gly Ser Cys Cys Leu Val Gly Val Ile Cys Ser Gly						
145		150		155		160
Thr Leu Tyr Val Ser Asn Leu Gly Asp Ser Arg Ala Val Leu Gly Thr						
	165			170		175
Leu Ser Lys Ala Thr Gly Glu Val Gln Ala Thr Gln Leu Ser Thr Glu						
	180			185		190
His Asn Ala Ser Phe Glu Ser Val Arg Arg Glu Leu Gln Ser Leu His						
	195			200		205
Pro Asp Asp Ser Gln Ile Val Val Leu Lys His Asn Val Trp Arg Val						
	210			215		220
Lys Gly Leu Ile Gln Ile Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys						
225		230		235		240
Lys Ala Glu Phe Asn Arg Glu Pro Leu Tyr Gln Lys Phe Arg Leu Arg						
	245			250		255
Glu Ala Phe Lys Arg Pro Ile Leu Ser Ser Glu Pro Glu Thr Thr Val						
	260			265		270
His Gln Leu Leu Pro His Asp Gln Phe Ile Ile Phe Ala Ser Asp Gly						
	275			280		285
Leu Trp Glu His Leu Ser Asn Gln Glu Ala Val Asp Leu Val Gln Lys						
	290			295		300
His Pro His Asn Gly Ile Ala Arg Arg Leu Val Lys Ala Ala Leu Gln						
305		310		315		320

Glu Ala Ala Lys Lys Arg Glu Met Arg Tyr Ser Asp Leu Lys Lys Ile  
325 330 335

Asp Arg Gly Val Arg Arg His Phe His Asp Asp Ile Thr Val Val Val  
340 345 350

Val Phe Leu Asp Ser His Leu Val Ser Arg Ala Ser Ser Val Arg Gly  
355 360 365

Pro Asn Ile Ser Val Lys Gly Gly Gly Ile Ser Leu Pro Pro Asn Ala  
370 375 380

Leu Ala Pro Cys Ala Thr Pro Thr Glu Pro Val Pro Asn  
385 390 395

&lt;210&gt; 35

<211> 743

## <212> DNA

<213> Mesembryanthemum crystallinum

**<220>**

**<221> CDS**

$\langle 222 \rangle$  (1) .. (420)

&lt;400&gt; 35

cct gag cta gca cct aaa gat ggg gat ttc cgt ttc aat atc tct gag 48  
Pro Glu Leu Ala Pro Lys Asp Gly Asp Phe Arg Phe Asn Ile Ser Glu  
1 5 10 15

cct gaa gct atg cta cca gct gga acf gta gat cat gcl gti gaa agg   96  
Leu Glu Ala Met Leu Pro Ala Gly Thr Val Asp His Ala Val Glu Arg

20                      25                      30

att tat caa gag atg ccg cgg tgg gaa gag act gtt tta ggt tcc agg 144  
Ile Tyr Gln Glu Met Pro Arg Trp Glu Glu Thr Val Leu Gly Ser Arg  
35 40 45

agc aga tat gag cat gtc att cag gca ctt gca gat aaa tac cct tca 192  
Ser Arg Tyr Glu His Val Ile Gln Ala Leu Ala Asp Lys Tyr Pro Ser  
50' 55 60

gaa aat ttg ttg cta gtt acg cat ggt gaa ggt gtt ggg act tca gtt 240  
Glu Asn Leu Leu Leu Val Thr His Gly Glu Gly Val Gly Thr Ser Val

65	70	75	80	
gca acg ttt ttg aaa ggc gct gtt gtt tat gaa gla aag tat tgt gct	288			
Ala Thr Phe Leu Lys Gly Ala Val Val Tyr Glu Val Lys Tyr Cys Ala				
85	90	95		
tat tca caa gca aca aga cgc atc agc tat gga gaa ggc gag tca ttt	336			
Tyr Ser Gln Ala Thr Arg Arg Ile Ser Tyr Gly Glu Gly Glu Ser Phe				
100	105	110		
act gct ggt acc ttt cag ttg gtc act gcc tca gac caa acc ggt att	384			
Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile				
115	120	125		
ggt tac tac aca tct agc agc ttg tct gat ggt gla tgacttaicg	430			
Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val				
130	135	140		
gaactcccca gtctctgcat tctgaaaggi gctttttagt ttccgaataa ttcttcaaat	490			
ccacatgica gaagatccat tctttaggic agatgtctat ctactgctcc cagccttagag	550			
ctgctcatgg gtattggcgc ccttctattt ttaggtagag tctttgagta agccttgcca	610			
catcaaggcc tcagattatt gaalgtacaa cagaataggi tglagcttca ttggctagta	670			
cagtgaccic tticatgggt ctgaaacaic aatataaagg ttigaatggc aaaaaaaaaa	730			
aaaaaaaaaa aaa	743			

&lt;210&gt; 36

&lt;211&gt; 140

&lt;212&gt; PRT

&lt;213&gt; Mesembryanthemum crystallinum

&lt;400&gt; 36

Pro	Glu	Leu	Ala	Pro	Lys	Asp	Gly	Asp	Phe	Arg	Phe	Asn	Ile	Ser	Glu
1				5				10						15	

Leu	Glu	Ala	Met	Leu	Pro	Ala	Gly	Thr	Val	Asp	His	Ala	Val	Glu	Arg
			20					25						30	

Ile	Tyr	Gln	Glu	Met	Pro	Arg	Trp	Glu	Glu	Thr	Val	Leu	Gly	Ser	Arg
			35					40						45	

Ser Arg Tyr Glu His Val Ile Gln Ala Leu Ala Asp Lys Tyr Pro Ser  
 50 55 60  
 Glu Asn Leu Leu Leu Val Thr His Gly Glu Gly Val Gly Thr Ser Val  
 65 70 75 80  
 Ala Thr Phe Leu Lys Gly Ala Val Val Tyr Glu Val Lys Tyr Cys Ala  
 85 90 95  
 Tyr Ser Gln Ala Thr Arg Arg Ile Ser Tyr Gly Glu Gly Glu Ser Phe  
 100 105 110  
 Thr Ala Gly Thr Phe Gln Leu Val Thr Ala Ser Asp Gln Thr Gly Ile  
 115 120 125  
 Gly Tyr Tyr Thr Ser Ser Ser Leu Ser Asp Gly Val  
 130 135 140

<210> 37  
 <211> 348  
 <212> DNA  
 <213> Sueada japonica

<220>  
 <221> CDS  
 <222> (1)..(246)

<400> 37  
 atc att gct ccc cta gct att ggt ttg atc gtt ggt gcc aac atc tta 48  
 Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu  
 1 5 10 15  
 gcc gga ggt gca ttt gat ggt gcc tca atg aac cct gcc gtc tct ttt 96  
 Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe  
 20 25 30  
 ggc ccc gcc gtg gtt agc tgg agc tgg gcc aac cac tgg gtc tac tgg 144  
 Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp  
 35 40 45  
 gca ggc cca ctc att ggt ggt gga ctt gct ggt ctc gtt tat gag ttt 192  
 Ala Gly Pro Leu Ile Gly Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe  
 50 55 60



atc ttt att ggt cac caa gag cca gct ccg gac tac cag aga ctg 240  
 Ile Phe Ile Gly His Gln Glu Pro Ala Ser Ala Asp Tyr Gln Arg Leu  
 65 70 75 80

tct gct taagaatttt aattctttgc cctagggaaa aatgtttcat gcatgtattt 296  
 Ser Ala

tggtaatttg ttgggtctaa aattttatga agggaaaaaa aaaaaaaaaa aa 348

<210> 38

<211> 82

<212> PRT

<213> Sueada japonica

<400> 38

Ile Ile Ala Pro Leu Ala Ile Gly Leu Ile Val Gly Ala Asn Ile Leu  
 1 5 10 15

Ala Gly Gly Ala Phe Asp Gly Ala Ser Met Asn Pro Ala Val Ser Phe  
 20 25 30

Gly Pro Ala Val Val Ser Trp Ser Trp Ala Asn His Trp Val Tyr Trp  
 35 40 45

Ala Gly Pro Leu Ile Gly Gly Gly Leu Ala Gly Leu Val Tyr Glu Phe  
 50 55 60

Ile Phe Ile Gly His Gln Glu Pro Ala Ser Ala Asp Tyr Gln Arg Leu  
 65 70 75 80

Ser Ala

<210> 39

<211> 1602

<212> DNA

<213> Sueada japonica

<220>

<221> CDS

<222> (1).. (1419)

<400> 39

cac acc gtt gat tta acc att gaa gct atg atg ctc gat tct caa gct	48
His Thr Val Asp Leu Thr Ile Glu Ala Met Met Leu Asp Ser Gln Ala	
1 5 10 15	
tct gat ctt gac aaa gaa gaa cgt cct gag att ctt tca atg ctt ccg	96
Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Met Leu Pro	
20 25 30	
cct ctt gaa gga aaa tgc ctc ttg gaa ctt ggg gct ggt att ggt cgt	144
Pro Leu Glu Gly Lys Cys Leu Leu Glu Leu Gly Ala Gly Ile Gly Arg	
35 40 45	
ttt act ggt gaa ttg gct gag aaa gct ggc cag gtt att gct ctg gat	192
Phe Thr Gly Glu Leu Ala Glu Lys Ala Gly Gln Val Ile Ala Leu Asp	
50 55 60	
ttc att gag agt gct atc aag aag aat gaa gla atc aat ggg cac tac	240
Phe Ile Glu Ser Ala Ile Lys Lys Asn Glu Val Ile Asn Gly His Tyr	
65 70 75 80	
aaa aat gtc aag ttt atg tgt gct gat gtg act tct ccc act ctc agt	288
Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr Ser Pro Thr Leu Ser	
85 90 95	
ttc cca cca cat tca ttg gat gtg ata ttc tcc aat tgg tta ctc atg	336
Phe Pro Pro His Ser Leu Asp Val Ile Phe Ser Asn Trp Leu Leu Met	
100 105 110	
tat ctt tct gat gaa gag gtg gaa aat ttg gtt gaa aga atg ttg aaa	384
Tyr Leu Ser Asp Glu Glu Val Glu Asn Leu Val Glu Arg Met Leu Lys	
115 120 125	
tgg ttg aag cca ggg ggt tac att ttc ttc aga gaa tct tgt ttc cat	432
Trp Leu Lys Pro Gly Gly Tyr Ile Phe Phe Arg Glu Ser Cys Phe His	
130 135 140	
caa tct ggg gat cac aaa cgc aaa agc aat ccc acc cac tac cgt gaa	480
Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro Thr His Tyr Arg Glu	
145 150 155 160	
cct agg ttc tac act aag gcc ttc aaa gag tgt cat ttg caa gat gga	528
Pro Arg Phe Tyr Thr Lys Ala Phe Lys Glu Cys His Leu Gln Asp Gly	
165 170 175	
tct gga aac tct tat gag ctc tcc cta ctt agc tgc aaa tgt att gga	576
Ser Gly Asn Ser Tyr Glu Leu Ser Leu Leu Ser Cys Lys Cys Ile Gly	

180	185	190	
gct tat gtc aga aac aag aaa aac cag aac cag att agt tgg ttg tgg			624
Ala Tyr Val Arg Asn Lys Lys Asn Gln Asn Gln Ile Ser Trp Leu Trp			
195	200	205	
caa aaa gtt gat tct aag gat gat aag ggg ttc cag cga ttt ctg gat			672
Gln Lys Val Asp Ser Lys Asp Asp Lys Gly Phe Gln Arg Phe Leu Asp			
210	215	220	
act agc cag tac aag tgt aat agc att ctg cga tat gag cgt gta ttt			720
Thr Ser Gln Tyr Lys Cys Asn Ser Ile Leu Arg Tyr Glu Arg Val Phe			
225	230	235	240
ggc cct ggt tat gtt agc act gga gga tat gaa acc acc aaa gag ttt			768
Gly Pro Gly Tyr Val Ser Thr Gly Gly Tyr Glu Thr Thr Lys Glu Phe			
245	250	255	
gtg tca atg ctg gac ttg aag cct ggc cag aag gtc ctg gat gtt ggt			816
Val Ser Met Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly			
260	265	270	
tgt gga att ggt gga ggt gac ttt tac atg gcg gag acc ttt gat gtt			864
Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Thr Phe Asp Val			
275	280	285	
gag gtt gtt gga ttt gat ctc tcc gtt aat atg att tcc ttt gcc ctt			912
Glu Val Val Gly Phe Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu			
290	295	300	
gag cgt tct att ggg ctt aaa tgt gct gtt gag ttt gag gta gca gat			960
Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu Phe Glu Val Ala Asp			
305	310	315	320
tgc acc aag ala aac tac cct gat aac tct ttt gat gtc atc tat agc			1008
Cys Thr Lys Ile Asn Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser			
325	330	335	
cgt gac acc att ctg cat att cag gac aag cct gcg ttg ttt aga tcc			1056
Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser			
340	345	350	
ttc tac aaa tgg ttg aag cca gga ggt aaa gtt cta atc agt gat tac			1104
Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr			
355	360	365	

tgc aag aaa gct ggt cca ccc tca cct gaa ttc gcc gct tac att aag 1152  
 Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys  
 370 375 380

cag agg gga tat gat ctc cat gat gta aag gaa tat ggg cag atg ctt 1200  
 Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu  
 385 390 395 400

aaa gat gct gga ttt gtt gat gtt ctt gcc gag gat aga act gag cag 1248  
 Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln  
 405 410 415

ttc att cga gtt cta cgg aag gaa cta gag act gtt gag aag gaa aag 1296  
 Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys  
 420 425 430

gat gtg ttc att agt gat ttc tct gag gag gat tac aat gac att gtt 1344  
 Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val  
 435 440 445

gga ggt tgg aat gat aag ttg cgg agg act gcc aag ggt gag caa cga 1392  
 Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg  
 450 455 460

tgg ggt ctg ttc gtt gcc aag aag aag tgaagaatca gttgccgcac 1439  
 Trp Gly Leu Phe Val Ala Lys Lys Lys  
 465 470

tggcactgic gatttccctag tattaatctt caatgttttc atgtaatgta ctctacatg 1499

taaaattgcc aataagtgc atttcgcaga ctgtaagaig attaatcata ttttaicitt 1559

taattaaatca tggatttatg caaaaaaaaaa aaaaaaaaaa aaa 1602

&lt;210&gt; 40

&lt;211&gt; 473

&lt;212&gt; PRT

&lt;213&gt; Sueada japonica

&lt;400&gt; 40

His Thr Val Asp Leu Thr Ile Glu Ala Met Met Leu Asp Ser Gln Ala  
 1 5 10 15

Ser Asp Leu Asp Lys Glu Glu Arg Pro Glu Ile Leu Ser Met Leu Pro  
 20 25 30

Pro Leu Glu Gly Lys Cys Leu Leu Glu Leu Gly Ala Gly Ile Gly Arg  
                   35                                  40                                  45

Phe Thr Gly Glu Leu Ala Glu Lys Ala Gly Gln Val Ile Ala Leu Asp  
                   50                                  55                                  60

Phe Ile Glu Ser Ala Ile Lys Lys Asn Glu Val Ile Asn Gly His Tyr  
                   65                                  70                                  75                                  80

Lys Asn Val Lys Phe Met Cys Ala Asp Val Thr Ser Pro Thr Leu Ser  
                                   85                                  90                                  95

Phe Pro Pro His Ser Leu Asp Val Ile Phe Ser Asn Trp Leu Leu Met  
                                   100                                  105                                  110

Tyr Leu Ser Asp Glu Glu Val Glu Asn Leu Val Glu Arg Met Leu Lys  
                   115                                  120                                  125

Trp Leu Lys Pro Gly Gly Tyr Ile Phe Phe Arg Glu Ser Cys Phe His  
                   130                                  135                                  140

Gln Ser Gly Asp His Lys Arg Lys Ser Asn Pro Thr His Tyr Arg Glu  
                   145                                  150                                  155                                  160

Pro Arg Phe Tyr Thr Lys Ala Phe Lys Glu Cys His Leu Gln Asp Gly  
                                   165                                  170                                  175

Ser Gly Asn Ser Tyr Glu Leu Ser Leu Leu Ser Cys Lys Cys Ile Gly  
                                   180                                  185                                  190

Ala Tyr Val Arg Asn Lys Lys Asn Gln Asn Gln Ile Ser Trp Leu Trp  
                   195                                  200                                  205

Gln Lys Val Asp Ser Lys Asp Asp Lys Gly Phe Gln Arg Phe Leu Asp  
                   210                                  215                                  220

Thr Ser Gln Tyr Lys Cys Asn Ser Ile Leu Arg Tyr Glu Arg Val Phe  
                   225                                  230                                  235                                  240

Gly Pro Gly Tyr Val Ser Thr Gly Gly Tyr Glu Thr Thr Lys Glu Phe  
                                   245                                  250                                  255

Val Ser Met Leu Asp Leu Lys Pro Gly Gln Lys Val Leu Asp Val Gly  
                   260                                  265                                  270

Cys Gly Ile Gly Gly Gly Asp Phe Tyr Met Ala Glu Thr Phe Asp Val  
 275 280 285

Glu Val Val Gly Phe Asp Leu Ser Val Asn Met Ile Ser Phe Ala Leu  
 290 295 300

Glu Arg Ser Ile Gly Leu Lys Cys Ala Val Glu Phe Glu Val Ala Asp  
 305 310 315 320

Cys Thr Lys Ile Asn Tyr Pro Asp Asn Ser Phe Asp Val Ile Tyr Ser  
 325 330 335

Arg Asp Thr Ile Leu His Ile Gln Asp Lys Pro Ala Leu Phe Arg Ser  
 340 345 350

Phe Tyr Lys Trp Leu Lys Pro Gly Gly Lys Val Leu Ile Ser Asp Tyr  
 355 360 365

Cys Lys Lys Ala Gly Pro Pro Ser Pro Glu Phe Ala Ala Tyr Ile Lys  
 370 375 380

Gln Arg Gly Tyr Asp Leu His Asp Val Lys Glu Tyr Gly Gln Met Leu  
 385 390 395 400

Lys Asp Ala Gly Phe Val Asp Val Leu Ala Glu Asp Arg Thr Glu Gln  
 405 410 415

Phe Ile Arg Val Leu Arg Lys Glu Leu Glu Thr Val Glu Lys Glu Lys  
 420 425 430

Asp Val Phe Ile Ser Asp Phe Ser Glu Glu Asp Tyr Asn Asp Ile Val  
 435 440 445

Gly Gly Trp Asn Asp Lys Leu Arg Arg Thr Ala Lys Gly Glu Gln Arg  
 450 455 460

Trp Gly Leu Phe Val Ala Lys Lys Lys  
 465 470

<210> 41

<211> 1251

<212> DNA

<213> Salsola komarovii

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1).. (933)

&lt;400&gt; 41

cag cca ttt ggc aca att aat gga tca ctt cgt gtt act gla caa ggt 48  
 Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly  
 1 5 10 15

gag gtc att gaa caa tct ttt gga gag gag cac ttg tgt ttt aga aca 96  
 Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr  
 20 25 30

tta cag cgg tac aca gct gcc aca ctt gag cat gga atg cat cca cca 144  
 Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro  
 35 40 45

alc tct cct aaa cca gaa tgg cgt gca ctt ttg gac gag atg gct gtt 192  
 Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val  
 50 55 60

gtt gcc acc aag gaa tac cgc tct gtt gtt ttt cat gag cct cgc ttt 240  
 Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe  
 65 70 75 80

gtc gag tac ttc cgc agt gct aca cca gag aca gag tat ggg cgt atg 288  
 Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met  
 85 90 95

aat att gga agc cgt cct gca aag aga aag cca gga gga gga att gaa 336  
 Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Gly Ile Glu  
 100 105 110

act ctg cgt gca att cct tgg ata ttt tct tgg aca caa acc agg ttt 384  
 Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe  
 115 120 125

cat tta cct gtg tgg ctt ggg gtt gga gca gct ttt aag cat gcc ctt 432  
 His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu  
 130 135 140

gac aag gac att aag aat ctt tct ata ctc aag gcc atg tat aat gag 480  
 Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu  
 145 150 155 160

tgg ccg ttc ttc aga gtg act att gat ctc tta gaa atg gtt ttc act 528

Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Leu Glu Met Val Phe Thr  
 165 170 175  
 aaa gga gac cct gga att gct gct tta tai gac aag ctt ctg gtg gca 576  
 Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ala  
 180 185 190  
 gag gat ttg aag ccc ttt ggg gaa aag ttg agg aaa agt ttc gaa gat 624  
 Glu Asp Leu Lys Pro Phe Gly Glu Lys Leu Arg Lys Ser Phe Glu Asp  
 195 200 205  
 acc aaa ctg ctt ctg ctt aag gtt gct ggg cac aag gag tta ctg gaa 672  
 Thr Lys Leu Leu Leu Leu Lys Val Ala Gly His Lys Glu Leu Leu Glu  
 210 215 220  
 gga gat cct tac ttg aaa cag aga ctg cga ctt cgt gat cct tac att 720  
 Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg Asp Pro Tyr Ile  
 225 230 235 240  
 aca acc ctt aat gtt ttc caa gca tat act ctg aag cgg atc cgt gat 768  
 Thr Thr Leu Asn Val Phe Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp  
 245 250 255  
 ccc aat ttc cat gta gct gaa ggg cca cac tta tcc aag gaa gta ttg 816  
 Pro Asn Phe His Val Ala Glu Gly Pro His Leu Ser Lys Glu Val Leu  
 260 265 270  
 gaa tca aac aat gct gag ctt gtg aag ctg aat cct act agt gag tat 864  
 Glu Ser Asn Asn Ala Glu Leu Val Lys Leu Asn Pro Thr Ser Glu Tyr  
 275 280 285  
 cct cct ggc ctt gag gac acc ctt atc ttg acc atg aag ggt att gct 912  
 Pro Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala  
 290 295 300  
 gct ggc atg cag aac acc ggt taactgacac ggtgtgcacg tctattgcaa 963  
 Ala Gly Met Gln Asn Thr Gly  
 305 310  
 ctattcctca actccttcctg gtttggggat ccgggctcgg agatagccat cgttgggtgat 1023  
 gtgcgtgatg agcacctaat tgtattcaaa gtcgttattt caagtcattt gttttgtat 1083  
 tttgttcttc tgtatgtttt tgttatttct acttaagggt gggttgtgtc acttgtgact 1143  
 aataccggac tgtgtaataa atgggtgttg tactgaagaa cagttgtttt tcttctacgt 1203



gagttatatt gatgagttta tcttttattt aaaaaaaaaa aaaaaaaaaa

1251

<210> 42

<211> 311

<212> PRT

<213> Salsola komarovii

<400> 42

Gln Pro Phe Gly Thr Ile Asn Gly Ser Leu Arg Val Thr Val Gln Gly  
1 5 10 15

Glu Val Ile Glu Gln Ser Phe Gly Glu Glu His Leu Cys Phe Arg Thr  
20 25 30

Leu Gln Arg Tyr Thr Ala Ala Thr Leu Glu His Gly Met His Pro Pro  
35 40 45

Ile Ser Pro Lys Pro Glu Trp Arg Ala Leu Leu Asp Glu Met Ala Val  
50 55 60

Val Ala Thr Lys Glu Tyr Arg Ser Val Val Phe His Glu Pro Arg Phe  
65 70 75 80

Val Glu Tyr Phe Arg Ser Ala Thr Pro Glu Thr Glu Tyr Gly Arg Met  
85 90 95

Asn Ile Gly Ser Arg Pro Ala Lys Arg Lys Pro Gly Gly Gly Ile Glu  
100 105 110

Thr Leu Arg Ala Ile Pro Trp Ile Phe Ser Trp Thr Gln Thr Arg Phe  
115 120 125

His Leu Pro Val Trp Leu Gly Val Gly Ala Ala Phe Lys His Ala Leu  
130 135 140

Asp Lys Asp Ile Lys Asn Leu Ser Ile Leu Lys Ala Met Tyr Asn Glu  
145 150 155 160

Trp Pro Phe Phe Arg Val Thr Ile Asp Leu Leu Glu Met Val Phe Thr  
165 170 175

Lys Gly Asp Pro Gly Ile Ala Ala Leu Tyr Asp Lys Leu Leu Val Ala  
180 185 190

Glu Asp Leu Lys Pro Phe Gly Glu Lys Leu Arg Lys Ser Phe Glu Asp  
 195 200 205

Thr Lys Leu Leu Leu Lys Val Ala Gly His Lys Glu Leu Leu Glu  
 210 215 220

Gly Asp Pro Tyr Leu Lys Gln Arg Leu Arg Leu Arg Asp Pro Tyr Ile  
 225 230 235 240

Thr Thr Leu Asn Val Phe Gln Ala Tyr Thr Leu Lys Arg Ile Arg Asp  
 245 250 255

Pro Asn Phe His Val Ala Glu Gly Pro His Leu Ser Lys Glu Val Leu  
 260 265 270

Glu Ser Asn Asn Ala Glu Leu Val Lys Leu Asn Pro Thr Ser Glu Tyr  
 275 280 285

Pro Pro Gly Leu Glu Asp Thr Leu Ile Leu Thr Met Lys Gly Ile Ala  
 290 295 300

Ala Gly Met Gln Asn Thr Gly  
 305 310

<210> 43

<211> 637

<212> DNA

<213> *Avicennia marina*

<220>

<221> CDS

<222> (1).. (339)

<400> 43

caa tac ttg gta aat gaa gtg aag aaa act gtt cag ggg cgt gct caa 48  
 Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln  
 1 5 10 15

ctt ggt gtg gaa gca ttt gct gat gcg ctt ctt gtg gtt cca aag acg 96  
 Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Leu Val Val Pro Lys Thr  
 20 25 30

ctt gcc gag aac tct ggc ctt gat acc cag gat ttg att att gaa ctt 144  
 Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu

35	40	45	
acg gga gaa tat gaa aaa ggg aat gtg gla gga ctt aat cta cac aca			192
Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr			
50	55	60	
gga gaa cct ata gat cct caa atg gag ggt atc ttt gac aat tat tcc			240
Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser			
65	70	75	80
gtg aag cgt cag atc ata aac tca ggc ccc gtt att gca tct cag ctg			288
Val Lys Arg Gln Ile Ile Asn Ser Gly Pro Val Ile Ala Ser Gln Leu			
85	90	95	
cta ctt gtc gac gag gtt att cgt gct ggt cgt aac atg cgt aaa ccg			336
Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro			
100	105	110	
aat tagctttcac cctagtlttt gtgatgttgg tgaagatggt aattttattt			389
Asn			
aggtagggtc atggttcctt ttgtttagcc taagcactat gtattcattg ccacttgaga			449
tttgaatttt gatcatcagg cggttgaact tticgccigi taaaaattgc accagaaatt			509
attcgaccat gggtatgcat ctacttgigt tgiaccigac ttggctaagt tatttgaaga			569
tacactcigt gctcagcaaa gaattggaaa aaaaggaatt gatltcatca aaaaaaaaaa			629
aaaaaaaa			637

&lt;210&gt; 44

&lt;211&gt; 113

&lt;212&gt; PRT

&lt;213&gt; Avicennia marina

&lt;400&gt; 44

Gln Tyr Leu Val Asn Glu Val Lys Lys Thr Val Gln Gly Arg Ala Gln
1 5 10 15

Leu Gly Val Glu Ala Phe Ala Asp Ala Leu Leu Val Val Pro Lys Thr
20 25 30

Leu Ala Glu Asn Ser Gly Leu Asp Thr Gln Asp Leu Ile Ile Glu Leu
35 40 45

Thr Gly Glu Tyr Glu Lys Gly Asn Val Val Gly Leu Asn Leu His Thr  
 50 55 60  
 Gly Glu Pro Ile Asp Pro Gln Met Glu Gly Ile Phe Asp Asn Tyr Ser  
 65 70 75 80  
 Val Lys Arg Gln Ile Ile Asn Ser Gly Pro Val Ile Ala Ser Gln Leu  
 85 90 95  
 Leu Leu Val Asp Glu Val Ile Arg Ala Gly Arg Asn Met Arg Lys Pro  
 100 105 110

Asn

<210> 45  
 <211> 741  
 <212> DNA  
 <213> *Avicennia marina*

<220>  
 <221> CDS  
 <222> (3).. (293)

<400> 45  
 aa gag atc aat tgt ctt gaa tgg gag aac ttt gct ttc cat ccc agc 47  
 Glu Ile Asn Cys Leu Glu Trp Glu Asn Phe Ala Phe His Pro Ser  
 1 5 10 15  
 cca ctc att gtt ctt gtt ttt gaa aga tac aac agg gca agt gat aac 95  
 Pro Leu Ile Val Leu Val Phe Glu Arg Tyr Asn Arg Ala Ser Asp Asn  
 20 25 30  
 tgg aaa gct ttg aag gag ttg gaa aag gcg gca gaa gtt tac tgg aag 143  
 Trp Lys Ala Leu Lys Glu Leu Glu Lys Ala Ala Glu Val Tyr Trp Lys  
 35 40 45  
 gca aaa gat cga ctg cct cct cgg acg gtc aag ata gat ata aac atc 191  
 Ala Lys Asp Arg Leu Pro Pro Arg Thr Val Lys Ile Asp Ile Asn Ile  
 50 55 60  
 gaa agg gat tta gca tat gca ctc aag gtt aaa gaa tgc ccg cag ata 239  
 Glu Arg Asp Leu Ala Tyr Ala Leu Lys Val Lys Glu Cys Pro Gln Ile

65                                      70                                      75  
 c i g t t c t t a c g c g g a a a c a g g a l a t t a t a c a g a g a g a a a g g t a g c c c a    287  
 Leu Phe Leu Arg Gly Asn Arg Ile Leu Tyr Arg Glu Lys Gly Ser Pro  
 80                                      85                                      90                                      95  
  
 t t t c t c t g a t a t t g c a t g t a c a t c a g a t c t t t c a a t c t g c a c c a g a a c c a a t t g a g    343  
 Phe Leu  
  
 t t t a c c a l c a t t t c c a g a a a t t a g a t c a t c g g a l g a a t t g g t t c a g a l g a t c g c g c a t t t    403  
 c t a t t a c a a t g c a a a a a a g c c t t c g t g c a t c g a t g a t g c a g c t t t c t c t t c a c c a c a t c a    463  
 c t g a a g g t g a g g t t g t c a a a t g g a a l c c a g c a t c a g t c a t t a g g g a g g a c t g a a g c t g t a    523  
 c g g a g g g a a g t g g t t t a a a t t c a g a t t g g a t c t t t g a a g t g g c a g t g g t g a t t g a a a c g    583  
 c c a a a a g t t t c t g a g g a a t a a c t t g t t g g g a t t t t g c a g t g a a c t g t a g t a a c t t t c t c    643  
 g c a t g t a a a a c t a g a c t t t c a t c a a t c a a c c a c c a a c c t t t a t g t a t a t g a a a c c t a t    703  
 g a g g t t g a a a t t t c t a g t t a    741

&lt;210&gt; 46

&lt;211&gt; 97

&lt;212&gt; PRT

&lt;213&gt; Avicennia marina

&lt;400&gt; 46

Glu Ile Asn Cys Leu Glu Trp Glu Asn Phe Ala Phe His Pro Ser Pro  
 1                                      5                                      10                                      15

Leu Ile Val Leu Val Phe Glu Arg Tyr Asn Arg Ala Ser Asp Asn Trp  
 20                                      25                                      30

Lys Ala Leu Lys Glu Leu Glu Lys Ala Ala Glu Val Tyr Trp Lys Ala  
 35                                      40                                      45

Lys Asp Arg Leu Pro Pro Arg Thr Val Lys Ile Asp Ile Asn Ile Glu  
 50                                      55                                      60

Arg Asp Leu Ala Tyr Ala Leu Lys Val Lys Glu Cys Pro Gln Ile Leu  
 65                                      70                                      75                                      80

Phe Leu Arg Gly Asn Arg Ile Leu Tyr Arg Glu Lys Gly Ser Pro Phe

85

90

95

Leu

&lt;210&gt; 47

&lt;211&gt; 983

&lt;212&gt; DNA

&lt;213&gt; Salsola komarovii

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1).. (762)

&lt;400&gt; 47

alg ttc ctt cat cac cac ttt tca tct tca tct tct tct ttt ctt ctt	48
Met Phe Leu His His His Phe Ser Ser Ser Ser Ser Ser Phe Leu Leu	
1 5 10 15	

ctc ttc ttc tct ctc cta ata ttc ctt tca tct gct aat ctt tat cat	96
Leu Phe Phe Ser Leu Leu Ile Phe Leu Ser Ser Ala Asn Leu Tyr His	
20 25 30	

cag aat caa gga tct tgt agt gac ttt gaa tca gaa cca tca atg gct	144
Gln Asn Gln Gly Ser Cys Ser Asp Phe Glu Ser Glu Pro Ser Met Ala	
35 40 45	

act ctt ggt gga ttg cgc gaa tcc cat ggt gct tct aat gat gct gag	192
Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu	
50 55 60	

att gaa acc ctt gct cgc ttt gct gtt gat gaa cac aac aaa aaa gag	240
Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu	
65 70 75 80	

aat gca ttg ttg gag ttt gca agg gtt gla aag gca aag gaa cag gtg	288
Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val	
85 90 95	

glt gcg ggt aca ttg cal cac ttc act aic gaa gca att gaa gcg ggc	336
Val Ala Gly Thr Leu His His Phe Thr Ile Glu Ala Ile Glu Ala Gly	
100 105 110	

aag aag aag ctc tac gaa gcg aag gtg tgg gtg aag cca tgg atg aac	384
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Lys	Lys	Lys	Leu	Tyr	Glu	Ala	Lys	Val	Trp	Val	Lys	Pro	Trp	Met	Asn		
		115						120					125				
ttt	aag	gag	ctg	cag	gaa	ttt	aag	cat	gct	gat	gaa	tcc	ccg	tca	alc	432	
Phe	Lys	Glu	Leu	Gln	Glu	Phe	Lys	His	Ala	Asp	Glu	Ser	Pro	Ser	Ile		
		130						135					140				
act	ccg	tcc	gac	ctc	ggc	gct	aat	aga	gaa	ggg	cat	tcg	gga	gga	tgg	480	
Thr	Pro	Ser	Asp	Leu	Gly	Ala	Asn	Arg	Glu	Gly	His	Ser	Gly	Gly	Trp		
		145						150					155		160		
aaa	gat	gig	ccg	gtc	cat	gac	ccg	gaa	gig	caa	aat	gca	gca	aat	cat	528	
Lys	Asp	Val	Pro	Val	His	Asp	Pro	Glu	Val	Gln	Asn	Ala	Ala	Asn	His		
					165					170					175		
gct	ctt	aag	acc	tig	caa	caa	aga	tcc	aac	tcc	tta	ttt	ccg	tat	gaa	576	
Ala	Leu	Lys	Thr	Leu	Gln	Gln	Arg	Ser	Asn	Ser	Leu	Phe	Pro	Tyr	Glu		
					180					185					190		
ctg	cag	gaa	gtt	gct	cat	gct	agg	gct	gag	gtt	ctg	gaa	gac	act	gcg	624	
Leu	Gln	Glu	Val	Ala	His	Ala	Arg	Ala	Glu	Val	Leu	Glu	Asp	Thr	Ala		
			195						200						205		
aag	ttt	aac	ctg	cac	ctc	aag	gig	aag	aga	gga	aac	aag	gat	gag	ttt	672	
Lys	Phe	Asn	Leu	His	Leu	Lys	Val	Lys	Arg	Gly	Asn	Lys	Asp	Glu	Phe		
		210						215							220		
ttc	aat	gig	gag	gig	cac	aaa	aac	agc	gaa	gga	aac	tac	aac	ctt	aat	720	
Phe	Asn	Val	Glu	Val	His	Lys	Asn	Ser	Glu	Gly	Asn	Tyr	Asn	Leu	Asn		
			225					230					235		240		
cag	atg	ggg	aac	gtt	gag	ccc	gag	gtt	gag	aaa	agt	agt	gtt			762	
Gln	Met	Gly	Asn	Val	Glu	Pro	Glu	Val	Glu	Lys	Ser	Ser	Val				
				245						250							
tagactcgtt	gaggggtgtg	taagtactcg	ttcgttaactt	ttcgtatggt	caggcaagta	822											
tggagtaagg	actagactac	tagtactagt	aagtacagct	gacttgggtt	gaglaaaata	882											
acctcgactt	tggttgcacc	atcatacttt	gtatgtttat	ggctttgtca	atgtatgtta	942											
agtgaagatt	gtttgcttga	lctaaaaaaa	aaaaaaaaaa	a		983											

&lt;210&gt; 48

&lt;211&gt; 254

&lt;212&gt; PRT

<213> *Salsola komarovii*

&lt;400&gt; 48

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Met Phe Leu His His His Phe Ser Ser Ser Ser Ser Ser Phe Leu Leu
  1           5           10           15

Leu Phe Phe Ser Leu Leu Ile Phe Leu Ser Ser Ala Asn Leu Tyr His
      20           25           30

Gln Asn Gln Gly Ser Cys Ser Asp Phe Glu Ser Glu Pro Ser Met Ala
      35           40           45

Thr Leu Gly Gly Leu Arg Glu Ser His Gly Ala Ser Asn Asp Ala Glu
      50           55           60

Ile Glu Thr Leu Ala Arg Phe Ala Val Asp Glu His Asn Lys Lys Glu
      65           70           75           80

Asn Ala Leu Leu Glu Phe Ala Arg Val Val Lys Ala Lys Glu Gln Val
      85           90           95

Val Ala Gly Thr Leu His His Phe Thr Ile Glu Ala Ile Glu Ala Gly
      100          105          110

Lys Lys Lys Leu Tyr Glu Ala Lys Val Trp Val Lys Pro Trp Met Asn
      115          120          125

Phe Lys Glu Leu Gln Glu Phe Lys His Ala Asp Glu Ser Pro Ser Ile
      130          135          140

Thr Pro Ser Asp Leu Gly Ala Asn Arg Glu Gly His Ser Gly Gly Trp
      145          150          155          160

Lys Asp Val Pro Val His Asp Pro Glu Val Gln Asn Ala Ala Asn His
      165          170          175

Ala Leu Lys Thr Leu Gln Gln Arg Ser Asn Ser Leu Phe Pro Tyr Glu
      180          185          190

Leu Gln Glu Val Ala His Ala Arg Ala Glu Val Leu Glu Asp Thr Ala
      195          200          205

Lys Phe Asn Leu His Leu Lys Val Lys Arg Gly Asn Lys Asp Glu Phe
      210          215          220

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Phe Asn Val Glu Val His Lys Asn Ser Glu Gly Asn Tyr Asn Leu Asn  
 225 230 235 240

Gln Met Gly Asn Val Glu Pro Glu Val Glu Lys Ser Ser Val  
 245 250

<210> 49

<211> 543

<212> DNA

<213> Salsola komarovii

<220>

<221> CDS

<222> (3).. (389)

<400> 49

aa aat aag gtt gac tta gct cga gat ttc acc ttc ata gac gac gtc 47  
 Asn Lys Val Asp Leu Ala Arg Asp Phe Thr Phe Ile Asp Asp Val  
 1 5 10 15

gta aag ggg tgc tta ggt tca ctg gat tct tcc ggt aag agt acc ggt 95  
 Val Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly  
 20 25 30

agc ggc ggt aaa aaa cgt ggg ccc gct ccg tac aga atc tac aac ttg 143  
 Ser Gly Gly Lys Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu  
 35 40 45

ggg aac act caa ccg gtc act gta ccg aca ctt gtc ggt atc cta gag 191  
 Gly Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu  
 50 55 60

aag cat ctc aaa gtt aag gcc aag aag aat gtg gtt gag atg ccc gga 239  
 Lys His Leu Lys Val Lys Ala Lys Lys Asn Val Val Glu Met Pro Gly  
 65 70 75

aat ggt gac gtg ccc ttc aca cat gcg aat atc tct ttg gcc cga aaa 287  
 Asn Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys  
 80 85 90 95

gat ttc ggg tat aaa ccc act acc gat ttg caa acc ggg ttg aaa aag 335  
 Asp Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys  
 100 105 110

ttt gtt aga tgg tat ctc act tat tac ggc tac aac aac ggc aag cct 383  
 Phe Val Arg Trp Tyr Leu Thr Tyr Tyr Gly Tyr Asn Asn Gly Lys Pro  
 115 120 125

gla aat taataataaa atataagtaa tttttttttt cttttttttt ataaattaca 439  
 Val Asn

gaattatttt ttttgggtgg tttatgaatt ttgttggata atatggggat tctttttttc 499

taaatgggaa aaataagaat ccaaggaaaa aaaaaaaaaa aaaa 543

<210> 50

<211> 129

<212> PRT

<213> Salsola komarovii

<400> 50

Asn Lys Val Asp Leu Ala Arg Asp Phe Thr Phe Ile Asp Asp Val Val  
 1 5 10 15

Lys Gly Cys Leu Gly Ser Leu Asp Ser Ser Gly Lys Ser Thr Gly Ser  
 20 25 30

Gly Gly Lys Lys Arg Gly Pro Ala Pro Tyr Arg Ile Tyr Asn Leu Gly  
 35 40 45

Asn Thr Gln Pro Val Thr Val Pro Thr Leu Val Gly Ile Leu Glu Lys  
 50 55 60

His Leu Lys Val Lys Ala Lys Lys Asn Val Val Glu Met Pro Gly Asn  
 65 70 75 80

Gly Asp Val Pro Phe Thr His Ala Asn Ile Ser Leu Ala Arg Lys Asp  
 85 90 95

Phe Gly Tyr Lys Pro Thr Thr Asp Leu Gln Thr Gly Leu Lys Lys Phe  
 100 105 110

Val Arg Trp Tyr Leu Thr Tyr Tyr Gly Tyr Asn Asn Gly Lys Pro Val  
 115 120 125

Asn

<210> 51  
 <211> 1219  
 <212> DNA  
 <213> Sueada japonica

<220>  
 <221> CDS  
 <222> (2).. (871)

<400> 51

c aca gga gca aac aaa gga ala gga ctt gaa cta tgc aaa caa cta gct 49  
 Thr Gly Ala Asn Lys Gly Ile Gly Leu Glu Leu Cys Lys Gln Leu Ala  
           1                  5                  10                  15

gct aaa gga gtt gta gta gtt ctc act tct aga gat gga aaa aga ggc 97  
 Ala Lys Gly Val Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly  
                   20                  25                  30

tta caa gct cat gaa aat ctc att aaa tct gga att aat cct gaa aat 145  
 Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn  
                   35                  40                  45

ctt cac ttt cat cag ctc gat gtt act gac atc act agt att gct gct 193  
 Leu His Phe His Gln Leu Asp Val Thr Asp Ile Thr Ser Ile Ala Ala  
                   50                  55                  60

att gct ggt ttc atc aat tcc aaa ttc ggc aaa ctt gat atc ctg gtg 241  
 Ile Ala Gly Phe Ile Asn Ser Lys Phe Gly Lys Leu Asp Ile Leu Val  
                   65                  70                  75                  80

aac aat gct gga att att gga gat atg gtt aac ttt gat gct tta ata 289  
 Asn Asn Ala Gly Ile Ile Gly Asp Met Val Asn Phe Asp Ala Leu Ile  
                   85                  90                  95

gca gca gga ttt ggc act cca aga gaa cag atc aat ctt gag gac agt 337  
 Ala Ala Gly Phe Gly Thr Pro Arg Glu Gln Ile Asn Leu Glu Asp Ser  
                   100                  105                  110

ccc ggg aca gta aca cag aca tat gag ctt acg aaa gaa tgc tta caa 385  
 Pro Gly Thr Val Thr Gln Thr Tyr Glu Leu Thr Lys Glu Cys Leu Gln  
                   115                  120                  125

aca aat tat tat gga gcg aaa aga acc gtt gaa gct ttg ctt ccg ctt 433  
 Thr Asn Tyr Tyr Gly Ala Lys Arg Thr Val Glu Ala Leu Leu Pro Leu  
                   130                  135                  140

ctc aag tta tcc gat tct cca agg att gtc aat gtc tcc tct ttt cta 481  
 Leu Lys Leu Ser Asp Ser Pro Arg Ile Val Asn Val Ser Ser Phe Leu  
 145 150 155 160

gga agg ttg acg tat ata cca aat gag acg atc aga ggg gtc cta aga 529  
 Gly Arg Leu Thr Tyr Ile Pro Asn Glu Thr Ile Arg Gly Val Leu Arg  
 165 170 175

gat gcc gag agc ctt aca gaa gaa cga ata gat gag att ctg aat gac 577  
 Asp Ala Glu Ser Leu Thr Glu Glu Arg Ile Asp Glu Ile Leu Asn Asp  
 180 185 190

atg ctg agg gac ttc aaa gac tgt tca ttc aaa gag aag gga tgg cct 625  
 Met Leu Arg Asp Phe Lys Asp Cys Ser Phe Lys Glu Lys Gly Trp Pro  
 195 200 205

aaa aat ctg gca gcc tat ata gtt tca aag gcg gcc ttg agt gca tac 673  
 Lys Asn Leu Ala Ala Tyr Ile Val Ser Lys Ala Ala Leu Ser Ala Tyr  
 210 215 220

aca aga ata ctg gct aag aaa tac cca tca atc atg atc aac tgt att 721  
 Thr Arg Ile Leu Ala Lys Lys Tyr Pro Ser Ile Met Ile Asn Cys Ile  
 225 230 235 240

tgc cct ggc ttt gtc aaa acf gac atc aat gga aac aca gga cac ttg 769  
 Cys Pro Gly Phe Val Lys Thr Asp Ile Asn Gly Asn Thr Gly His Leu  
 245 250 255

ccg gtt gaa gaa ggt gca gcg agt ctg gca agg tta gcg ttg atg ccc 817  
 Pro Val Glu Glu Gly Ala Ala Ser Leu Ala Arg Leu Ala Leu Met Pro  
 260 265 270

caa att tta cct tct gga cta ttc ttt cag aga acf gaa gtt tct tctg 865  
 Gln Ile Leu Pro Ser Gly Leu Phe Phe Gln Arg Thr Glu Val Ser Ser  
 275 280 285

ttt gaa taaaacaatt tgcctattca aaccaacacc acatactat gaagtltcca 921  
 Phe Glu  
 290

ttgttaggca tctttacgaa aaaaataaga catctgcaat acigtltactg gaaaatgcaa 981

tgtacttttt tcatgtatgc atggcgcagt tatttattct gacigcaaca ataagattct 1041

gtlttttcaa ggcactctaa ggaatgctga igtaccgttc tcaaacaagc agacaagtag 1101

acacgttga ttgcatgtc ttcatcgtc caatcattt gigtltgtat gttagcatg 1161

tttaactaat tacaagagtg taattaaagat caacttttat aaaaaaaaaa aaaaaaaa 1219

<210> 52

<211> 290

<212> PRT

<213> Sueada japonica

<400> 52

Thr Gly Ala Asn Lys Gly Ile Gly Leu Glu Leu Cys Lys Gln Leu Ala  
1 5 10 15

Ala Lys Gly Val Val Val Val Leu Thr Ser Arg Asp Gly Lys Arg Gly  
20 25 30

Leu Gln Ala His Glu Asn Leu Ile Lys Ser Gly Ile Asn Pro Glu Asn  
35 40 45

Leu His Phe His Gln Leu Asp Val Thr Asp Ile Thr Ser Ile Ala Ala  
50 55 60

Ile Ala Gly Phe Ile Asn Ser Lys Phe Gly Lys Leu Asp Ile Leu Val  
65 70 75 80

Asn Asn Ala Gly Ile Ile Gly Asp Met Val Asn Phe Asp Ala Leu Ile  
85 90 95

Ala Ala Gly Phe Gly Thr Pro Arg Glu Gln Ile Asn Leu Glu Asp Ser  
100 105 110

Pro Gly Thr Val Thr Gln Thr Tyr Glu Leu Thr Lys Glu Cys Leu Gln  
115 120 125

Thr Asn Tyr Tyr Gly Ala Lys Arg Thr Val Glu Ala Leu Leu Pro Leu  
130 135 140

Leu Lys Leu Ser Asp Ser Pro Arg Ile Val Asn Val Ser Ser Phe Leu  
145 150 155 160

Gly Arg Leu Thr Tyr Ile Pro Asn Glu Thr Ile Arg Gly Val Leu Arg  
165 170 175

Asp Ala Glu Ser Leu Thr Glu Glu Arg Ile Asp Glu Ile Leu Asn Asp

	180		185		190										
Met	Leu	Arg	Asp	Phe	Lys	Asp	Cys	Ser	Phe	Lys	Glu	Lys	Gly	Trp	Pro
	195						200					205			
Lys	Asn	Leu	Ala	Ala	Tyr	Ile	Val	Ser	Lys	Ala	Ala	Leu	Ser	Ala	Tyr
	210					215					220				
Thr	Arg	Ile	Leu	Ala	Lys	Lys	Tyr	Pro	Ser	Ile	Met	Ile	Asn	Cys	Ile
225					230					235				240	
Cys	Pro	Gly	Phe	Val	Lys	Thr	Asp	Ile	Asn	Gly	Asn	Thr	Gly	His	Leu
				245					250					255	
Pro	Val	Glu	Glu	Gly	Ala	Ala	Ser	Leu	Ala	Arg	Leu	Ala	Leu	Met	Pro
		260						265					270		
Gln	Ile	Leu	Pro	Ser	Gly	Leu	Phe	Phe	Gln	Arg	Thr	Glu	Val	Ser	Ser
	275						280					285			
Phe	Glu														
	290														

<210> 53  
 <211> 1148  
 <212> DNA  
 <213> Sueada japonica

<220>  
 <221> CDS  
 <222> (3).. (848)

<400> 53

ga	agc	agg	ccg	gal	atc	cat	glt	gaa	caa	gct	cat	tca	gat	gat	att	47
Ser	Arg	Pro	Asp	Ile	His	Val	Glu	Gln	Ala	His	Ser	Asp	Asp	Ile		
1				5					10					15		

act	ggg	tig	aaa	ttc	tca	tgt	gat	ggt	cgt	cat	cig	tig	tct	aga	agt	95
Thr	Gly	Leu	Lys	Phe	Ser	Cys	Asp	Gly	Arg	His	Leu	Leu	Ser	Arg	Ser	
		20						25					30			

ttt	gat	tgc	aca	ctt	aag	glt	tgg	gac	tig	cgc	caa	atg	aag	cgg	tct	143
Phe	Asp	Cys	Thr	Leu	Lys	Val	Trp	Asp	Leu	Arg	Gln	Met	Lys	Arg	Ser	
		35					40						45			

ctt aag gtg ttt gat gaa tta cca aat cac tat gct caa acg aat gtc 191  
 Leu Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val  
           50                          55                          60

tca ttt agt cca gat gag cag ctc atc ttg act ggt aca tct gta gaa 239  
 Ser Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu  
           65                          70                          75

agg gat agc cca act gga gga ttg ttg tgc ttt tat gat cgg gaa aaa 287  
 Arg Asp Ser Pro Thr Gly Gly Leu Leu Cys Phe Tyr Asp Arg Glu Lys  
           80                          85                          90                          95

ctt gaa cta gta tca aaa gtt ggc att tct cct act tgc agt gtt gtg 335  
 Leu Glu Leu Val Ser Lys Val Gly Ile Ser Pro Thr Cys Ser Val Val  
                           100                          105                          110

caa tgt gcc tgg cac cca agg ctg aal cag gtt ttt gcc act gct gga 383  
 Gln Cys Ala Trp His Pro Arg Leu Asn Gln Val Phe Ala Thr Ala Gly  
                           115                          120                          125

aat aaa agc caa gga ggt aca cat gta ctc tat gat cca acc atg agt 431  
 Asn Lys Ser Gln Gly Gly Thr His Val Leu Tyr Asp Pro Thr Met Ser  
           130                          135                          140

gag aga ggt gct ctt gtg tgt gtt gct cgt gca cca agg atg aaa tca 479  
 Glu Arg Gly Ala Leu Val Cys Val Ala Arg Ala Pro Arg Met Lys Ser  
           145                          150                          155

gtg gat gat ttt gag gtg cag ccg gtt ata cat aac cct cac gca ctt 527  
 Val Asp Asp Phe Glu Val Gln Pro Val Ile His Asn Pro His Ala Leu  
           160                          165                          170                          175

ccc ttg ttc aga gat cag cca agc cgc aaa cgt caa aga gag aag att 575  
 Pro Leu Phe Arg Asp Gln Pro Ser Arg Lys Arg Gln Arg Glu Lys Ile  
                           180                          185                          190

ctg aag gac cca ata aaa tcc cac aaa cca gag ctt cct atg tca gga 623  
 Leu Lys Asp Pro Ile Lys Ser His Lys Pro Glu Leu Pro Met Ser Gly  
                           195                          200                          205

cct ggc cat ggt ggc aga act ggt aca tca tct ggt agt ttg tta aca 671  
 Pro Gly His Gly Gly Arg Thr Gly Thr Ser Ser Gly Ser Leu Leu Thr  
           210                          215                          220

caa tat ctc ctc aag caa ggg ggc atg ttg aaa gag aca tgg atg gat 719

Gln Tyr Leu Leu Lys Gln Gly Gly Met Leu Lys Glu Thr Trp Met Asp  
 225 230 235  
 gaa gat ccc aga gaa gct att ctc aag tai gct gat gct gca gaa aag 767  
 Glu Asp Pro Arg Glu Ala Ile Leu Lys Tyr Ala Asp Ala Ala Glu Lys  
 240 245 250 255  
 gat cca aag ttt att gcc ccg gct tai gct gag act cag ccc aag cca 815  
 Asp Pro Lys Phe Ile Ala Pro Ala Tyr Ala Glu Thr Gln Pro Lys Pro  
 260 265 270  
 glc ttt gag gat tct gat aag gaa gat gaa gaa taattcatct ttgcagtagg 868  
 Val Phe Glu Asp Ser Asp Lys Glu Asp Glu Glu  
 275 280  
 ttggattaat ttaatttgag aatattatc tgtgtatatt aatagccaat tttcaggcg 928  
 aatgataatgc ttctcacatt aatgctgag ttttatttgc tgctacagat tglagatgaa 988  
 taggttaaig taaacacaag catagagatt agaatalaga aatgattcig tatccaaaac 1048  
 acaattttat caccagatgg tatcaaaagc tgtattgact gttagagtaat gtcattaaacc 1108  
 actttcactc cccaaaaaaa aaaaaaaaaa aaaaaaaaaa 1148

&lt;210&gt; 54

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Sueada japonica

&lt;400&gt; 54

Ser Arg Pro Asp Ile His Val Glu Gln Ala His Ser Asp Asp Ile Thr  
 1 5 10 15

Gly Leu Lys Phe Ser Cys Asp Gly Arg His Leu Leu Ser Arg Ser Phe  
 20 25 30

Asp Cys Thr Leu Lys Val Trp Asp Leu Arg Gln Met Lys Arg Ser Leu  
 35 40 45

Lys Val Phe Asp Glu Leu Pro Asn His Tyr Ala Gln Thr Asn Val Ser  
 50 55 60

Phe Ser Pro Asp Glu Gln Leu Ile Leu Thr Gly Thr Ser Val Glu Arg  
 65 70 75 80



Asp Ser Pro Thr Gly Gly Leu Leu Cys Phe Tyr Asp Arg Glu Lys Leu  
                             85                            90                            95  
 Glu Leu Val Ser Lys Val Gly Ile Ser Pro Thr Cys Ser Val Val Gln  
                             100                            105                            110  
 Cys Ala Trp His Pro Arg Leu Asn Gln Val Phe Ala Thr Ala Gly Asn  
                             115                            120                            125  
 Lys Ser Gln Gly Gly Thr His Val Leu Tyr Asp Pro Thr Met Ser Glu  
                             130                            135                            140  
 Arg Gly Ala Leu Val Cys Val Ala Arg Ala Pro Arg Met Lys Ser Val  
                             145                            150                            155                            160  
 Asp Asp Phe Glu Val Gln Pro Val Ile His Asn Pro His Ala Leu Pro  
                             165                            170                            175  
 Leu Phe Arg Asp Gln Pro Ser Arg Lys Arg Gln Arg Glu Lys Ile Leu  
                             180                            185                            190  
 Lys Asp Pro Ile Lys Ser His Lys Pro Glu Leu Pro Met Ser Gly Pro  
                             195                            200                            205  
 Gly His Gly Gly Arg Thr Gly Thr Ser Ser Gly Ser Leu Leu Thr Gln  
                             210                            215                            220  
 Tyr Leu Leu Lys Gln Gly Gly Met Leu Lys Glu Thr Trp Met Asp Glu  
                             225                            230                            235                            240  
 Asp Pro Arg Glu Ala Ile Leu Lys Tyr Ala Asp Ala Ala Glu Lys Asp  
                             245                            250                            255  
 Pro Lys Phe Ile Ala Pro Ala Tyr Ala Glu Thr Gln Pro Lys Pro Val  
                             260                            265                            270  
 Phe Glu Asp Ser Asp Lys Glu Asp Glu Glu  
                             275                            280

&lt;210&gt; 55

&lt;211&gt; 1193

&lt;212&gt; DNA

&lt;213&gt; Avicennia marina

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (3).. (815)

&lt;400&gt; 55

gi	gca	cc	gag	tta	ctt	ctt	gga	gca	aag	cat	taa	aca	agt	gct	gtt	47
Ala	Pro	Glu	Leu	Leu	Leu	Gly	Ala	Lys	His	Tyr	Thr	Ser	Ala	Val		
1				5					10					15		

gac	aig	tgg	gct	gtg	ggc	tgc	att	ttt	gct	gag	ctt	ctg	act	cta	aag	95
Asp	Met	Trp	Ala	Val	Gly	Cys	Ile	Phe	Ala	Glu	Leu	Leu	Thr	Leu	Lys	
			20					25					30			

cca	cta	ttt	caa	ggg	caa	gaa	gta	aaa	ggg	act	tct	aat	cca	ttt	cag	143
Pro	Leu	Phe	Gln	Gly	Gln	Glu	Val	Lys	Gly	Thr	Ser	Asn	Pro	Phe	Gln	
			35					40					45			

ctt	gat	caa	ctt	gac	aaa	atc	ttt	aag	gtc	cta	ggt	cat	ccc	acg	caa	191
Leu	Asp	Gln	Leu	Asp	Lys	Ile	Phe	Lys	Val	Leu	Gly	His	Pro	Thr	Gln	
	50					55						60				

gaa	aag	tgg	ccc	aca	cta	gcg	aat	ctt	cca	cat	tgg	cag	tct	gat	gtg	239
Glu	Lys	Trp	Pro	Thr	Leu	Ala	Asn	Leu	Pro	His	Trp	Gln	Ser	Asp	Val	
	65					70					75					

caa	cgt	atc	caa	ggg	cic	aaa	tac	gac	aat	act	gga	ctt	tac	aat	gtt	287
Gln	Arg	Ile	Gln	Gly	Leu	Lys	Tyr	Asp	Asn	Thr	Gly	Leu	Tyr	Asn	Val	
	80				85					90				95		

gtt	cat	ctc	tcc	ccc	aaa	aat	cca	gca	tat	gac	ctt	ctc	tca	aag	atg	335
Val	His	Leu	Ser	Pro	Lys	Asn	Pro	Ala	Tyr	Asp	Leu	Leu	Ser	Lys	Met	
				100				105					110			

ctt	gag	tat	gat	cc	aga	aaa	aga	ata	aca	gct	aca	caa	gct	ctt	gag	383
Leu	Glu	Tyr	Asp	Pro	Arg	Lys	Arg	Ile	Thr	Ala	Thr	Gln	Ala	Leu	Glu	
			115				120					125				

cat	gag	tat	ttt	cgc	atg	gaa	cc	ttg	ccg	gga	cgc	aac	gct	ctg	gta	431
His	Glu	Tyr	Phe	Arg	Met	Glu	Pro	Leu	Pro	Gly	Arg	Asn	Ala	Leu	Val	
	130					135				140						

cca	cca	cag	cc	ggg	gag	aaa	att	gtg	aac	tac	cca	aca	cga	cca	gtg	479
Pro	Pro	Gln	Pro	Gly	Glu	Lys	Ile	Val	Asn	Tyr	Pro	Thr	Arg	Pro	Val	
	145				150					155						

gac aca aat act gal aat gaa gga aca atc agc ctc cag ccc tct caa 527  
 Asp Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln  
 160 165 170 175

ccg gta tca tct ggg aat tct gtg tct ggg gcc cta gcc ggt cct cat 575  
 Pro Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His  
 180 185 190

gla atg caa aat aga tcc atg cct cgg cca atg ccc atg gtt ggc gtg 623  
 Val Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val  
 195 200 205

caa cgc atg caa cct cca ggg atc cca cac tat ggt ctt gct tct cag 671  
 Gln Arg Met Gln Pro Pro Gly Ile Pro His Tyr Gly Leu Ala Ser Gln  
 210 215 220

gca gga atg ggt gga gta aat cct ggt ggc atc cca att cag cgg gga 719  
 Ala Gly Met Gly Gly Val Asn Pro Gly Gly Ile Pro Ile Gln Arg Gly  
 225 230 235

gtt cct gct cag gct cat caa cag cag cag atg aga agg aaa gac cct 767  
 Val Pro Ala Gln Ala His Gln Gln Gln Gln Met Arg Arg Lys Asp Pro  
 240 245 250 255

gga atg ggg atg act gga tat cct cca caa cag aaa tca agg cgc ttt 815  
 Gly Met Gly Met Thr Gly Tyr Pro Pro Gln Gln Lys Ser Arg Arg Phe  
 260 265 270

tgagagtcg ggtggattg gagcctaagi gggaggacaa atacacattc caatcaaat 875  
 agaggaaacc ttaaatlaa cttccagtca gctgaaacga caccagtgga accaaatgat 935  
 ctgaccccat ticcaggatt gcatgattt attaggagga alacacgaat gaagattcga 995  
 gtctaglgcc aaattatct aacatacct catcattgt tctactaca ticcagcgtt 1055  
 atatgtttca actagtgga ggtttctgc agtccacca tgtggcaca aalgattca 1115  
 tagcatgcca agcaacatt tactgggtg taccaaggca atttctctat ticcaagcca 1175  
 aaaaaaaaa aaaaaaaaa 1193

&lt;210&gt; 56

&lt;211&gt; 271

&lt;212&gt; PRT

<213> Avicennia marina

<400> 56

Ala Pro Glu Leu Leu Leu Gly Ala Lys His Tyr Thr Ser Ala Val Asp  
1 5 10 15

Met Trp Ala Val Gly Cys Ile Phe Ala Glu Leu Leu Thr Leu Lys Pro  
20 25 30

Leu Phe Gln Gly Gln Glu Val Lys Gly Thr Ser Asn Pro Phe Gln Leu  
35 40 45

Asp Gln Leu Asp Lys Ile Phe Lys Val Leu Gly His Pro Thr Gln Glu  
50 55 60

Lys Trp Pro Thr Leu Ala Asn Leu Pro His Trp Gln Ser Asp Val Gln  
65 70 75 80

Arg Ile Gln Gly Leu Lys Tyr Asp Asn Thr Gly Leu Tyr Asn Val Val  
85 90 95

His Leu Ser Pro Lys Asn Pro Ala Tyr Asp Leu Leu Ser Lys Met Leu  
100 105 110

Glu Tyr Asp Pro Arg Lys Arg Ile Thr Ala Thr Gln Ala Leu Glu His  
115 120 125

Glu Tyr Phe Arg Met Glu Pro Leu Pro Gly Arg Asn Ala Leu Val Pro  
130 135 140

Pro Gln Pro Gly Glu Lys Ile Val Asn Tyr Pro Thr Arg Pro Val Asp  
145 150 155 160

Thr Asn Thr Asp Ile Glu Gly Thr Ile Ser Leu Gln Pro Ser Gln Pro  
165 170 175

Val Ser Ser Gly Asn Ser Val Ser Gly Ala Leu Ala Gly Pro His Val  
180 185 190

Met Gln Asn Arg Ser Met Pro Arg Pro Met Pro Met Val Gly Val Gln  
195 200 205

Arg Met Gln Pro Pro Gly Ile Pro His Tyr Gly Leu Ala Ser Gln Ala  
210 215 220

Gly Met Gly Gly Val Asn Pro Gly Gly Ile Pro Ile Gln Arg Gly Val

225		230		235		240									
Pro	Ala	Gln	Ala	His	Gln	Gln	Gln	Gln	Met	Arg	Arg	Lys	Asp	Pro	Gly
				245					250					255	
Met	Gly	Met	Thr	Gly	Tyr	Pro	Pro	Gln	Gln	Lys	Ser	Arg	Arg	Phe	
			260					265					270		

<210> 57  
 <211> 1195  
 <212> DNA  
 <213> Sueada japonica

<220>  
 <221> CDS  
 <222> (116).. (1195)

<400> 57

gcaaaaglaa gagtgaaaga acacaaacca actttctiatt ttacagctcaa atcaaattca 60  
 atagtggaac aacaatagag ggcaaattct cattgcccaa ttcaaatttg gtaaa atg 118  
 Met  
 1  
 gct caa aag cat ttg aaa gaa ctt ctc aaa gaa gat caa gaa ccc ttt 166  
 Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro Phe  
 5 10 15  
 cat tta aag gat tac att gca act aaa aaa tgt caa ctt ttg aag aag 214  
 His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys Lys  
 20 25 30  
 caa gaa tta gla gla ccc aaa tca aaa ctt caa ctc aaa aag cca aag 262  
 Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro Lys  
 35 40 45  
 cca aaa cca att tca aaa agc act tca gtt ttg tgc aaa aat gct tgc 310  
 Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala Cys  
 50 55 60 65  
 ttt tta tct tta caa gaa tcc cct gac ctc aga aaa tcc ccc aaa cta 358  
 Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys Leu  
 70 75 80

ttt gat ttt cca cct tcc cct gtt tct aac aaa agc cca aac aga gta	406
Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg Val	
85 90 95	
ttc ctc aat gtt cct gct aaa act gct gct ctt ctt ctt gaa gct gct	454
Phe Leu Asn Val Pro Ala Lys Thr Ala Ala Leu Leu Leu Glu Ala Ala	
100 105 110	
att cga att caa acc cac aaa tct aaa ccc aaa acc cag att aaa aat	502
Ile Arg Ile Gln Thr His Lys Ser Lys Pro Lys Thr Gln Ile Lys Asn	
115 120 125	
tgc ggt ttt ggg cta ttc ggg tca atg tta aag cga tta aat ctt cga	550
Ser Gly Phe Gly Leu Phe Gly Ser Met Leu Lys Arg Leu Asn Leu Arg	
130 135 140 145	
aat cgt acc caa aaa atc aag tca aaa aca gag gaa caa aac aga gga	598
Asn Arg Thr Gln Lys Ile Lys Ser Lys Thr Glu Glu Gln Asn Arg Gly	
150 155 160	
tgc tct gtt ttg agg agt gtt gaa gaa gaa aaa act acc acc att tct	646
Cys Ser Val Leu Arg Ser Val Glu Glu Glu Lys Thr Thr Thr Ile Ser	
165 170 175	
tct tct tca tct tca tct tct tca aca tca tgc tat tct tgc tgt tct	694
Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Tyr Ser Ser Cys Ser	
180 185 190	
tgc aat gag agg tta agt agt ttg gat ttg gag agt tct agc agt gga	742
Cys Asn Glu Arg Leu Ser Ser Leu Asp Leu Glu Ser Ser Ser Ser Gly	
195 200 205	
aga tca tta cat gat gaa gat gaa gat gaa gat gaa gat gaa ttt	790
Arg Ser Leu His Asp Glu Asp Glu Asp Glu Asp Glu Asp Asp Glu Phe	
210 215 220 225	
gag ttt aca aat gtt tta aga gaa aat aat aat gat gat aaa aat gga	838
Glu Phe Thr Asn Val Leu Arg Glu Asn Asn Asn Asp Asp Lys Asn Gly	
230 235 240	
ggc tat tat tca gga att tgc tta agt cct ttg agt cca ttt cgt ttt	886
Gly Tyr Tyr Ser Gly Ile Cys Leu Ser Pro Leu Ser Pro Phe Arg Phe	
245 250 255	
gct ctt cat aaa aac tct tct cct gaa cgt tgc tct cct gct aaa tcc	934
Ala Leu His Lys Asn Ser Ser Pro Glu Arg Cys Ser Pro Ala Lys Ser	

260	265	270	
cct gtt cgt tgc aaa ttt gag ggt aat gct aaa tat gaa caa gaa agc			982
Pro Val Arg Cys Lys Phe Glu Gly Asn Ala Lys Tyr Glu Gln Glu Ser			
275	280	285	
tta ata aag ttt gaa gac gaa gat gaa gaa gac aaa gag caa aat agc			1030
Leu Ile Lys Phe Glu Asp Glu Asp Glu Glu Asp Lys Glu Gln Asn Ser			
290	295	300	305
cct gtt tcc gtg ctg gat cct cca ttc gag gat gat tac gat ggg cat			1078
Pro Val Ser Val Leu Asp Pro Pro Phe Glu Asp Asp Tyr Asp Gly His			
310	315	320	
gag gag gat agc tac gag gac atc gaa tgc agc tat gct ttt gta caa			1126
Glu Glu Asp Ser Tyr Glu Asp Ile Glu Cys Ser Tyr Ala Phe Val Gln			
325	330	335	
aga gca caa caa gag tta ttg cac aga ctt cac cgg ttc cag aag cia			1174
Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys Leu			
340	345	350	
gcg gag ttg gac cca att gaa			1195
Ala Glu Leu Asp Pro Ile Glu			
355	360		

<210> 58  
 <211> 360  
 <212> PRT  
 <213> Sueada japonica

<400> 58  
 Met Ala Gln Lys His Leu Lys Glu Leu Leu Lys Glu Asp Gln Glu Pro  
 1 5 10 15  
 Phe His Leu Lys Asp Tyr Ile Ala Thr Lys Lys Cys Gln Leu Leu Lys  
 20 25 30  
 Lys Gln Glu Leu Val Val Pro Lys Ser Lys Leu Gln Leu Lys Lys Pro  
 35 40 45  
 Lys Pro Lys Pro Ile Ser Lys Ser Thr Ser Val Leu Cys Lys Asn Ala  
 50 55 60  
 Cys Phe Leu Ser Leu Gln Glu Ser Pro Asp Leu Arg Lys Ser Pro Lys

65		70		75		80
Leu Phe Asp Phe Pro Pro Ser Pro Val Ser Asn Lys Ser Pro Asn Arg						
	85		90			95
Val Phe Leu Asn Val Pro Ala Lys Thr Ala Ala Leu Leu Leu Glu Ala						
	100		105			110
Ala Ile Arg Ile Gln Thr His Lys Ser Lys Pro Lys Thr Gln Ile Lys						
	115		120			125
Asn Ser Gly Phe Gly Leu Phe Gly Ser Met Leu Lys Arg Leu Asn Leu						
	130		135			140
Arg Asn Arg Thr Gln Lys Ile Lys Ser Lys Thr Glu Glu Gln Asn Arg						
	145		150			160
Gly Cys Ser Val Leu Arg Ser Val Glu Glu Glu Lys Thr Thr Thr Ile						
	165		170			175
Ser Ser Ser Ser Ser Ser Ser Ser Ser Thr Ser Ser Tyr Ser Ser Cys						
	180		185			190
Ser Cys Asn Glu Arg Leu Ser Ser Leu Asp Leu Glu Ser Ser Ser Ser						
	195		200			205
Gly Arg Ser Leu His Asp Glu Asp Glu Asp Glu Asp Glu Asp Asp Glu						
	210		215			220
Phe Glu Phe Thr Asn Val Leu Arg Glu Asn Asn Asn Asp Asp Lys Asn						
	225		230			240
Gly Gly Tyr Tyr Ser Gly Ile Cys Leu Ser Pro Leu Ser Pro Phe Arg						
	245		250			255
Phe Ala Leu His Lys Asn Ser Ser Pro Glu Arg Cys Ser Pro Ala Lys						
	260		265			270
Ser Pro Val Arg Cys Lys Phe Glu Gly Asn Ala Lys Tyr Glu Gln Glu						
	275		280			285
Ser Leu Ile Lys Phe Glu Asp Glu Asp Glu Glu Asp Lys Glu Gln Asn						
	290		295			300
Ser Pro Val Ser Val Leu Asp Pro Pro Phe Glu Asp Asp Tyr Asp Gly						
	305		310			320



His Glu Glu Asp Ser Tyr Glu Asp Ile Glu Cys Ser Tyr Ala Phe Val  
                                   325                                  330                                  335

Gln Arg Ala Gln Gln Glu Leu Leu His Arg Leu His Arg Phe Gln Lys  
                                   340                                  345                                  350

Leu Ala Glu Leu Asp Pro Ile Glu  
                                   355                                  360

<210> 59

<211> 1301

<212> DNA

<213> Salsola komarovii

<220>

<221> CDS

<222> (3).. (815)

<400> 59

gt gag gtt gac gat agc gtt aat agt cta cag gca gat gtt gac aac 47  
   Glu Val Asp Asp Ser Val Asn Ser Leu Gln Ala Asp Val Asp Asn  
           1                                  5                                  10                                  15

ctt tca att gag gaa cgc aga ttg gat gaa cag ata agg gaa atg caa 95  
   Leu Ser Ile Glu Glu Arg Arg Leu Asp Glu Gln Ile Arg Glu Met Gln  
                                   20                                  25                                  30

gaa aga ttg agg gaa atg agt gaa gat gat atc aat cag aag tgg ctt 143  
   Glu Arg Leu Arg Glu Met Ser Glu Asp Asp Ile Asn Gln Lys Trp Leu  
                                   35                                  40                                  45

ttt gta act gaa gaa gac ata aag ggt tta cct tgt ttt cag aat gaa 191  
   Phe Val Thr Glu Glu Asp Ile Lys Gly Leu Pro Cys Phe Gln Asn Glu  
                                   50                                  55                                  60

acc tta att gca att aaa gct cca cat gga aca act ttg gag gtt cca 239  
   Thr Leu Ile Ala Ile Lys Ala Pro His Gly Thr Thr Leu Glu Val Pro  
                                   65                                  70                                  75

gat cca gat gag gct gtc gat tat cct caa aga aga tac aag ata gtt 287  
   Asp Pro Asp Glu Ala Val Asp Tyr Pro Gln Arg Arg Tyr Lys Ile Val  
                                   80                                  85                                  90                                  95

ctt agg agc aca atg ggt cct att gat gta tat tta gtc agt caa ttt 335  
 Leu Arg Ser Thr Met Gly Pro Ile Asp Val Tyr Leu Val Ser Gln Phe  
                     100                    105                    110

gaa gag aag ttt gag gag atc agt ggt gct gac ggt cca cta agt ata 383  
 Glu Glu Lys Phe Glu Glu Ile Ser Gly Ala Asp Gly Pro Leu Ser Ile  
                     115                    120                    125

cca agt acc tca ggt gat gac aaa cac aca act gtt gca gct aag gaa 431  
 Pro Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu  
                     130                    135                    140

gaa agc aat ggc aat gag att gaa ata gaa gga caa ggg acc cat aga 479  
 Glu Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg  
                     145                    150                    155

atc tgc tca gat tcc aac gct cag caa gac ttt gtg agt gga att atg 527  
 Ile Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met  
 160                    165                    170                    175

aag ala gtg cct gaa gtt gat agt gat gca gat tac tgg ttg cta tcg 575  
 Lys Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser  
                     180                    185                    190

gat gct gat gtt agc att act gac atg tgg gga act gat tct gga gtt 623  
 Asp Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val  
                     195                    200                    205

gaa tgg aat gaa tta ggg act ala cat gaa gac tat gcc gtg gct aat 671  
 Glu Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn  
                     210                    215                    220

gtt ggc act tca cag cca caa agt cca cca aca agt gca aca gaa gtg 719  
 Val Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val  
                     225                    230                    235

ctt cca gct aac atg aca agc agg aga ttg aca tgg agt ttt gag aga 767  
 Leu Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg  
 240                    245                    250                    255

att gcc aar att cat tca aat ggt cac tat tgc ttg gaa gtg agg ctc 815  
 Ile Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu  
                     260                    265                    270

taactttcta ttattcalcc tgggatttgg gtacgaaagt ctgccttgaa gatgctgtaa 875

catgttgggt attacaactg tgtgaalcta gtaagttggg aggglgagat tgttcctgat 935  
 ctatattcac agccgggtgg gagagattga tgcctcaaca actgacaaaa ttggggcatg 995  
 ttaacggata gtaatgcagtt gtaattttgt acaacacatt tttgatattt agtcagtaca 1055  
 tcataactag cttctcciat acttcttcaa ttgcaactg gaatagattt ttagattaat 1115  
 tagatctctc ttgtatgga aatgtttcag ggtaacaagc cagaaattaa aatggtttta 1175  
 tggtaaaaaa tatatactta aattgtttgt aggaagtllc tgaagggttg ttggaaggct 1235  
 tttacaactt acaatgata aggaatttcg taccacaaat tcacaatgaa aaaaaaaaaa 1295  
 aaaaaa 1301

&lt;210&gt; 60

&lt;211&gt; 271

&lt;212&gt; PRT

&lt;213&gt; Salsola komarovii

&lt;400&gt; 60

Glu	Val	Asp	Asp	Ser	Val	Asn	Ser	Leu	Gln	Ala	Asp	Val	Asp	Asn	Leu
1				5				10						15	
Ser	Ile	Glu	Glu	Arg	Arg	Leu	Asp	Glu	Gln	Ile	Arg	Glu	Met	Gln	Glu
		20				25						30			
Arg	Leu	Arg	Glu	Met	Ser	Glu	Asp	Asp	Ile	Asn	Gln	Lys	Trp	Leu	Phe
		35				40						45			
Val	Thr	Glu	Glu	Asp	Ile	Lys	Gly	Leu	Pro	Cys	Phe	Gln	Asn	Glu	Thr
	50				55						60				
Leu	Ile	Ala	Ile	Lys	Ala	Pro	His	Gly	Thr	Thr	Leu	Glu	Val	Pro	Asp
65				70					75					80	
Pro	Asp	Glu	Ala	Val	Asp	Tyr	Pro	Gln	Arg	Arg	Tyr	Lys	Ile	Val	Leu
				85				90						95	
Arg	Ser	Thr	Met	Gly	Pro	Ile	Asp	Val	Tyr	Leu	Val	Ser	Gln	Phe	Glu
		100						105					110		
Glu	Lys	Phe	Glu	Glu	Ile	Ser	Gly	Ala	Asp	Gly	Pro	Leu	Ser	Ile	Pro
	115						120					125			

Ser Thr Ser Gly Asp Asp Lys His Thr Thr Val Ala Ala Lys Glu Glu  
 130 135 140  
 Ser Asn Gly Asn Glu Ile Glu Ile Glu Gly Gln Gly Thr His Arg Ile  
 145 150 155 160  
 Cys Ser Asp Ser Asn Ala Gln Gln Asp Phe Val Ser Gly Ile Met Lys  
 165 170 175  
 Ile Val Pro Glu Val Asp Ser Asp Ala Asp Tyr Trp Leu Leu Ser Asp  
 180 185 190  
 Ala Asp Val Ser Ile Thr Asp Met Trp Gly Thr Asp Ser Gly Val Glu  
 195 200 205  
 Trp Asn Glu Leu Gly Thr Ile His Glu Asp Tyr Ala Val Ala Asn Val  
 210 215 220  
 Gly Thr Ser Gln Pro Gln Ser Pro Pro Thr Ser Ala Thr Glu Val Leu  
 225 230 235 240  
 Pro Ala Asn Met Thr Ser Arg Arg Leu Thr Trp Ser Phe Glu Arg Ile  
 245 250 255  
 Ala Lys Ile His Ser Asn Gly His Tyr Cys Leu Glu Val Arg Leu  
 260 265 270

<210> 61  
 <211> 1032  
 <212> DNA  
 <213> *Salsola komarovii*

<220>  
 <221> CDS  
 <222> (1).. (732)

<400> 61  
 cca caa cga aga ccc gac ccg gtc ccg aac ctt cac ggt cag ctt ttt 48  
 Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe  
 1 5 10 15  
 caa cac cga aat cca cac cac cgt gac ctc cac ccc tgc cgt agc ccg 96  
 Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro

	20	25	30	
gca atg ggt cca ctc cct ccg cag act cat ctg cgc tgg tat tcc ctc				144
Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu				
	35	40	45	
tcg cgc tac tcc ccc gtc atc ggc ctc ggc gtc caa tgg aag ccc tcc				192
Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser				
	50	55	60	
tcc acc tca gct gcc act ctt caa ctc agc atc gac aaa aag tgc ctc				240
Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu				
	65	70	75	80
atc ttc caa ctc tcc cac tcc ccc gcc atc ccc gcc acc ctc cgc gac				288
Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp				
	85	90	95	
ctc ctc ctc gac gat cgc gtc acc ttc ttt ggt gtc cac aac gcc cgt				336
Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg				
	100	105	110	
gcc cgc gac ctc ctc caa ggg tcc cac cat gag ctc gac gtc aac aat				384
Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn				
	115	120	125	
ctg gtt gat ctt gcc gag gag gaa aat ggt cat tac ttg aag tgg tcc				432
Leu Val Asp Leu Ala Glu Glu Glu Asn Gly His Tyr Leu Lys Trp Ser				
	130	135	140	
atg gaa gac atg gct gaa gat gtg ttg ggc ttt tgt ggg gta cac aaa				480
Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys				
	145	150	155	160
ccc agg aag gtt atg tta agt ggt tgg gat cag tat tgc ttg tct aat				528
Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn				
	165	170	175	
gac cag gtt cag tat gct tgt gtt gat gct tac gtt tct ctt cgt ctt				576
Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu				
	180	185	190	
gct cga gct tat ggg tac cac cgt ctc gat cac gat gat gat tat gat				624
Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp				
	195	200	205	

gac cat gac gac gat gat aac gac cac acc gat gat gat tac gat gac 672  
 Asp His Asp Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp  
 210 215 220

gtt tac gac cgc aat ala ggc tct gat gat gat ggt tat gat gcc gat 720  
 Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Asp Gly Tyr Asp Ala Asp  
 225 230 235 240

gat gat cga cga tcatcaattt ggactagact tcgttatagg aagggtccga 772  
 Asp Asp Arg Arg

tcatcatgcc agtctaatla caaagagaca agaaataaaa atgatgatca aaaaaagaag 832

tcaatccata tacgtaatit tcatlgcaat atcaattitg aggtgittta ttatlgccct 892

giaataalag ttttatitaa taatagcact atagatctca tcttaacctt tacttatagg 952

gcttatgcgc tgaatgcca ataaccaagt ttaattitit tcatgatctg atgattactg 1012

caaaaaaaaa aaaaaaaaaa 1032

<210> 62

<211> 244

<212> PRT

<213> Salsola komarovii

<400> 62

Pro Gln Arg Arg Pro Asp Pro Val Pro Asn Leu His Gly Gln Leu Phe  
 1 5 10 15

Gln His Arg Asn Pro His His Arg Asp Leu His Pro Cys Arg Ser Pro  
 20 25 30

Ala Met Gly Pro Leu Pro Pro Gln Thr His Leu Arg Trp Tyr Ser Leu  
 35 40 45

Ser Arg Tyr Ser Pro Val Ile Gly Leu Gly Val Gln Trp Lys Pro Ser  
 50 55 60

Ser Thr Ser Ala Ala Thr Leu Gln Leu Ser Ile Asp Lys Lys Cys Leu  
 65 70 75 80

Ile Phe Gln Leu Ser His Ser Pro Ala Ile Pro Ala Thr Leu Arg Asp  
 85 90 95

Leu Leu Leu Asp Asp Arg Val Thr Phe Phe Gly Val His Asn Gly Arg  
 100 105 110

Ala Arg Asp Leu Leu Gln Gly Ser His His Glu Leu Asp Val Asn Asn  
 115 120 125

Leu Val Asp Leu Ala Glu Glu Glu Asn Gly His Tyr Leu Lys Trp Ser  
 130 135 140

Met Glu Asp Met Ala Glu Asp Val Leu Gly Phe Cys Gly Val His Lys  
 145 150 155 160

Pro Arg Lys Val Met Leu Ser Gly Trp Asp Gln Tyr Cys Leu Ser Asn  
 165 170 175

Asp Gln Val Gln Tyr Ala Cys Val Asp Ala Tyr Val Ser Leu Arg Leu  
 180 185 190

Ala Arg Ala Tyr Gly Tyr His Arg Leu Asp His Asp Asp Asp Tyr Asp  
 195 200 205

Asp His Asp Asp Asp Asp Asn Asp His Thr Asp Asp Asp Tyr Asp Asp  
 210 215 220

Val Tyr Asp Arg Asn Ile Gly Ser Asp Asp Asp Gly Tyr Asp Ala Asp  
 225 230 235 240

Asp Asp Arg Arg

<210> 63

<211> 1029

<212> DNA

<213> Mesembryanthemum crystallinum

<220>

<221> CDS

<222> (3).. (824)

<400> 63

ca cal atc agc cac atc cac tta att ccc cac agt ctt agt ctc tta 47  
 His Ile Ser His Ile His Leu Ile Pro His Ser Leu Ser Leu Leu  
 1 5 10 15

gac acc cal ctt agt ctt aag cct ctc atg gcc acc gcg gta ttc tca	95
Asp Thr His Leu Ser Leu Lys Pro Leu Met Ala Thr Ala Val Phe Ser	
20 25 30	
ccf tct gcc ctt cia tcc acc tcc aca tcc acc tca aca acc cct ctt	143
Pro Ser Ala Leu Leu Ser Thr Ser Thr Ser Thr Ser Thr Thr Pro Leu	
35 40 45	
aaa gct ccc ccc ttg gcc tta acc aag acc cac gta acg atc cca tca	191
Lys Ala Pro Pro Leu Ala Leu Thr Lys Thr His Val Thr Ile Pro Ser	
50 55 60	
tca tca aag cca ccc cia acc aat tta act acc agt tta act gct gtc	239
Ser Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val	
65 70 75	
gcc aca gct gct gcc ata atc ctg tcc aca acc cct cca tcc ttt gct	287
Ala Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala	
80 85 90 95	
gat gat ttg cag aca aat gca tac aac att tac tac ggc act gct gca	335
Asp Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala	
100 105 110	
agt gca gcc aat tat gga ggc tac ggt ggc aat tcc aac aag aaa gat	383
Ser Ala Ala Asn Tyr Gly Gly Tyr Gly Gly Asn Ser Asn Lys Lys Asp	
115 120 125	
tca gct gag tac ata tat gac glc cct gca ggt tgg aaa gag aga cta	431
Ser Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu	
130 135 140	
gta tca aaa gtt gag aag ggt acc aat gga aca gat agt gag ttc ttc	479
Val Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe	
145 150 155	
aac ccc aag aag aag aca gag cga gag tac ctt acc tac ctt gct ggt	527
Asn Pro Lys Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly	
160 165 170 175	
att agg caa cia ggt ccc aaa gaa gig atc ctc aac aac tta gca ctc	575
Ile Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu	
180 185 190	
tca gat gig aac ctg caa gat caa att tcc agt gca gac tct gtg aca	623
Ser Asp Val Asn Leu Gln Asp Gln Ile Ser Ser Ala Asp Ser Val Thr	



195	200	205	
tca gaa gag agg aaa gat gac aag gga cag gtt tac tat gat tat gag			671
Ser Glu Glu Arg Lys Asp Asp Lys Gly Gln Val Tyr Tyr Asp Tyr Glu			
210	215	220	
att gct gga gct ggt tca cac agt ttg ata tcg gta aca tgt gcc agg			719
Ile Ala Gly Ala Gly Ser His Ser Leu Ile Ser Val Thr Cys Ala Arg			
225	230	235	
aac aag cta tal gcg cat ttt gtt agc gca cca aca ccc gaa tgg aat			767
Asn Lys Leu Tyr Ala His Phe Val Ser Ala Pro Thr Pro Glu Trp Asn			
240	245	250	255
cgg gat caa gat atg ctg agg cac atc cac aac tca ttt aca aca gtc			815
Arg Asp Gln Asp Met Leu Arg His Ile His Asn Ser Phe Thr Thr Val			
260	265	270	
ggg tca ttc tagaaagigt atatgataat catttataga gatgicagag			864
Gly Ser Phe			
aggcatacat ttgaatgtac ttctgatgag ctggacttct tgatctatgt aacattgtaa			924
cgaaaattct ttctgggila tcagaaacct agtgagtgct tgaaacttgc aatgagaaac			984
tcctcaataa acaatgactt gtaacaaaa aaaaaaaaaa aaaaa			1029

&lt;210&gt; 64

&lt;211&gt; 274

&lt;212&gt; PRT

&lt;213&gt; Mesembryanthemum crystallinum

&lt;400&gt; 64

His	Ile	Ser	His	Ile	His	Leu	Ile	Pro	His	Ser	Leu	Ser	Leu	Leu	Asp
1				5				10					15		

Thr	His	Leu	Ser	Leu	Lys	Pro	Leu	Met	Ala	Thr	Ala	Val	Phe	Ser	Pro
		20					25					30			

Ser	Ala	Leu	Leu	Ser	Thr	Ser	Thr	Ser	Thr	Ser	Thr	Thr	Pro	Leu	Lys
	35					40						45			

Ala	Pro	Pro	Leu	Ala	Leu	Thr	Lys	Thr	His	Val	Thr	Ile	Pro	Ser	Ser
	50				55						60				

Ser Lys Pro Pro Leu Thr Asn Leu Thr Thr Ser Leu Thr Ala Val Ala  
 65 70 75 80  
 Thr Ala Ala Ala Ile Ile Leu Ser Thr Thr Pro Pro Ser Phe Ala Asp  
 85 90 95  
 Asp Leu Gln Thr Asn Ala Tyr Asn Ile Tyr Tyr Gly Thr Ala Ala Ser  
 100 105 110  
 Ala Ala Asn Tyr Gly Gly Tyr Gly Gly Asn Ser Asn Lys Lys Asp Ser  
 115 120 125  
 Ala Glu Tyr Ile Tyr Asp Val Pro Ala Gly Trp Lys Glu Arg Leu Val  
 130 135 140  
 Ser Lys Val Glu Lys Gly Thr Asn Gly Thr Asp Ser Glu Phe Phe Asn  
 145 150 155 160  
 Pro Lys Lys Lys Thr Glu Arg Glu Tyr Leu Thr Tyr Leu Ala Gly Ile  
 165 170 175  
 Arg Gln Leu Gly Pro Lys Glu Val Ile Leu Asn Asn Leu Ala Leu Ser  
 180 185 190  
 Asp Val Asn Leu Gln Asp Gln Ile Ser Ser Ala Asp Ser Val Thr Ser  
 195 200 205  
 Glu Glu Arg Lys Asp Asp Lys Gly Gln Val Tyr Tyr Asp Tyr Glu Ile  
 210 215 220  
 Ala Gly Ala Gly Ser His Ser Leu Ile Ser Val Thr Cys Ala Arg Asn  
 225 230 235 240  
 Lys Leu Tyr Ala His Phe Val Ser Ala Pro Thr Pro Glu Trp Asn Arg  
 245 250 255  
 Asp Gln Asp Met Leu Arg His Ile His Asn Ser Phe Thr Thr Val Gly  
 260 265 270  
 Ser Phe

&lt;210&gt; 65

&lt;211&gt; 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 65

gcctcgagaa ccgtctagac ttagatgaag gtg

33

<210> 66

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 66

tcctcgttc atctcgagct attacagctc

30